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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:15:32 ; Search time 38 Seconds  
(without alignments)  
1230.815 Million cell updates/sec

Title: US-09-944-807-2  
Perfect score: 1817  
Sequence: 1 METNFTPLNEVEVSYESA.....TNDTAANSASPPATELQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	23 AAU79035	Human formyl pepti
2	1811	99.7	351	22 ABB56354	Non-endogenous hum
3	1244.5	68.5	350	22 ABB56353	Non-endogenous hum
4	1157.5	63.7	343	23 AA021656	Mouse protein homo
5	1117	61.5	315	15 AAR48713	G-protein coupled
6	1117	61.5	315	17 AAR48713	G-protein coupled
7	554.5	30.5	356	21 AAU90678	Human G protein-co
8	553.5	30.5	356	21 AAU90678	Human G protein-co
9	542.5	29.9	477	22 AAU72389	Mouse C3a receptor
10	542.5	29.9	477	23 AAU75166	Mouse anaphylatoxi

11	542	29.8	372	20 AAW86323	Kidney injury asso
12	509.5	28.0	482	18 AAW23367	Novel G-protein co
13	509.5	28.0	482	19 AAW42376	Homo sapiens C3a r
14	509.5	28.0	482	23 AAU99102	Human anaphylotoxi
15	508.5	28.0	482	17 AAU02151	Human G-protein co
16	508.5	28.0	482	18 AAU06540	C5a-like seven tra
17	508	28.0	355	22 AAW93557	Human polypeptide,
18	507	27.9	350	22 ABB56337	Non-endogenous hum
19	507	27.9	363	22 AAW55822	Human bone marrow
20	507	27.9	363	22 AAW68196	Human bone marrow
21	507	27.9	363	22 AAW16016	Peptide #2454 enco
22	506.5	27.9	363	22 AAW28517	Peptide #2554 enco
23	506.5	27.9	482	22 ABB56336	Non-endogenous hum
24	504.5	27.8	485	21 AAW58319	Lung cancer associ
25	500	27.5	355	22 AAU01300	Human G-protein re
26	499.5	27.5	395	19 AAW44703	Human Th2/B19, Ho
27	499	27.5	355	21 AAU90609	Human G-protein re
28	497	27.5	355	22 AAU01299	Human G-protein re
29	497	27.4	355	21 AAW90643	Human mutant G pro
30	496	27.3	355	22 AAU01301	Human G-protein re
31	491	27.0	355	22 AAU01302	Human G-protein re
32	479	26.4	304	15 AAR48714	G-protein coupled
33	479	26.4	304	17 AAW02686	G-protein coupled
34	431.5	23.7	360	16 AAR80953	Recombinant high a
35	430.5	23.7	1064	16 AAR70124	IL8-R type 2-GBP 1
36	428.5	23.6	355	23 AAW80485	Gorilla CXCR2 rece
37	427.5	23.5	360	23 AAU01558	Human interleukin
38	426.5	23.5	355	14 AAR33420	Human IL-8 recepto
39	426.5	23.5	355	17 AAB09990	Human IL-8 recepto
40	426.5	23.5	355	23 AAW80482	Human CXCR2 recept
41	426.5	23.5	355	23 AAW80483	Chimpanzee CXCR2 r
42	426.5	23.5	359	21 AAB02844	Human G protein co
43	426.5	23.5	359	23 AAU02951	Protein of the ang
44	426.5	23.5	359	23 AAU78654	Human Angiotensin
45	426.5	23.5	360	13 AAR28273	Sequence in a low

## ALIGNMENTS

### RESULT 1

AAU79035  
ID AAU79035 standard; Protein; 351 AA.

AC AAU79035;

DT 18-JUN-2002 (first entry)

DE Human formyl peptide receptor like-1 receptor, FPRL-1.

XX Human; FPRL-1; formyl peptide receptor like-1; receptor;

KW ILM receptor; macrophage surface receptor; antiinflammatory; pulmonary;

KW chronic inflammatory airway disease; chronic bronchitis;

KW chronic obstructive pulmonary disease; COPD.

XX Homo sapiens.

XX WO200218938-A1.

XX 07-MAR-2002.

XX 23-AUG-2001; 2001WO-EP09727.

XX 01-SEP-2000; 2000GB-0021484.

XX (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.

XX Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;  
Weith A;

XX WPI; 2002-315580/35.

XX N-PSDB; ABB48101.

PT Determining an expression level of ILM (a macrophage surface receptor),  
PT for the diagnosis or monitoring of chronic inflammatory airway disease,  
PT comprises determining the level of the ILM receptor expressed in a  
PT macrophage -

XX Claim 7; Page 49-51; 79pp; English.

PS The invention relates to determining an expression level of an ILM  
XX receptor (macrophage surface receptor), comprises determining the level  
CC of an ILM receptor expressed in a macrophage. Also included are a method  
CC of determining whether a substance is an activator or an inhibitor of an  
CC ILM receptor, involving applying the substance to a test system which  
CC generates a measurable read-out upon modulation of the ILM receptor or an  
CC ILM receptor function, a test system for determining whether a substance  
CC is an activator or an inhibitor of an ILM receptor function,  
CC characterised in that the receptor is involved in a chronic inflammatory  
CC airway disease and where the receptor plays a role in mediating  
CC inflammation comprising: (i) an ILM receptor; (ii) an expression vector  
CC capable of expressing an ILM receptor in a cell; or (iii) a host cell  
CC transformed with an expression vector capable of expressing the ILM  
CC receptor and a substance determined to be an activator or inhibitor of an  
CC ILM receptor. The methods are useful for the diagnosis or monitoring of a  
CC chronic inflammatory airway disease, e.g. chronic bronchitis and chronic  
CC obstructive pulmonary disease (COPD). The substance determined to  
CC be an activator or inhibitor of an ILM receptor, is useful for treating  
CC the diseases and for modulating an ILM receptor, in a macrophage.  
CC The present sequence is an ILM receptor which is differentially  
CC expressed and which is involved in causing the induction and/or  
CC maintenance of the hyperactive status of macrophages involved in an  
CC inflammatory process.

XX Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 23; Length 351;  
Best Local Similarity 100.0%; Pred. No. 9.5e-196;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60  
DB 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60  
QY 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICVLPVMAQNHRTVSLAMKVIVGWPWILALVLTLPVFLFTVTPNGDTCYCTNF 180  
DB 121 LDRICVLPVMAQNHRTVSLAMKVIVGWPWILALVLTLPVFLFTVTPNGDTCYCTNF 180  
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKKGMIKSSRPL 240  
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKKGMIKSSRPL 240  
QY 241 RVLTVAVASFFICWPFQVALLGTWVWKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTVAVASFFICWPFQVALLGTWVWKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300  
QY 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351  
DB 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351

RESULT 2  
ABB56354 standard; Protein: 351 AA.

XX ABB56354;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 501.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;

KW constitutively activated GPCR; agonist; disease.

XX Homo sapiens.

OS Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US11098.

XX 07-APR-2000; 2000US-195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

XX N-PSDB; ABI97990.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
PT disease treatment, comprises contacting candidate compounds with  
PT versions of GPCRs -

XX Claim 1; Page 301-302; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous  
CC constitutively activated versions of known GPCRs are used in the  
CC invention for the direct identification of candidate compounds as  
CC receptor agonists, inverse agonists or partial agonists. Such  
CC agonists are useful as therapeutic agents for diseases or disorders  
CC associated with GPCRs. The present sequence is a non-endogenous  
CC version of a known human GPCR.

XX Sequence 351 AA;

Query Match 99.7%; Score 1811; DB 22; Length 351;  
Best Local Similarity 99.7%; Pred. No. 4.5e-195;  
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60  
DB 1 METNFTPLNEEVEEYESAGYTVLRILPLVGLVTVFVGLVGLNGLVIVWAGFRMTRVT 60  
QY 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TICYNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICVLPVMAQNHRTVSLAMKVIVGWPWILALVLTLPVFLFTVTPNGDTCYCTNF 180  
DB 121 LDRICVLPVMAQNHRTVSLAMKVIVGWPWILALVLTLPVFLFTVTPNGDTCYCTNF 180  
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKKGMIKSSRPL 240  
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKHKKGMIKSSRPL 240  
QY 241 RVLTVAVASFFICWPFQVALLGTWVWKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTVAVASFFICWPFQVALLGTWVWKEMLFYKGYKIIDLNVNPTSSLAFFNSCLNPM 300  
QY 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351  
DB 301 LYVFGQDFRERLIHSLPTSLSRALSEDSAPTNDTAANSASPPAETELQAM 351

RESULT 3

ABB56353

XX ABB56353 standard; Protein: 350 AA.

XX ABB56353;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 499.  
DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
KW constitutively activated GPCR; agonist; disease.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200177172-A2.  
PN 18-OCT-2001.  
XX 05-APR-2001; 2001WO-US11098.  
XX 07-APR-2000; 2000US-195747P.  
XX (AREN-) ARENA PHARM INC.  
XX Lehmann-Brunisma K, Liaw CW, Lin I;  
PI WPI; 2001-648759/74.  
XX N-PSDB; ABI97989.  
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
PT disease treatment, comprises contacting candidate compounds with  
PT versions of GPCRs -  
XX Claim 1; Page 299-300; 394pp; English.  
XX The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous  
CC constitutively activated versions of known GPCRs are used in the  
CC invention for the direct identification of candidate compounds as  
CC receptor agonists, inverse agonists or partial agonists. Such  
CC agonists are useful as therapeutic agents for diseases or disorders  
CC associated with GPCRs. The present sequence is a non-endogenous  
CC version of a known human GPCR.  
XX  
XX Sequence 350 AA;  
Query Match 68.5%; Score 1244.5; DB 22; Length 350;  
Best Local Similarity 68.6%; Pred. No. 2.8e-131;  
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;  
QY 1 METNEFTPLNEYRVSYESAGTYVLRILPLVVLGVTFVLGVLGSLVWAGFRMTFTVT 60  
Db 1 METNSSLPTNISGGTPAVSAGYLELDIITYLVFAVTFVLGVLGSLVWAGFRMTFTVT 60  
Y 61 TICVLNLALADSFETATLPFLIVSWMAGEKWPFGWFLCKLHIHVVDINLFGSVFLIGPIA 120  
Db 61 TISVLNLAVADFCFTSTLPFFMVRKAMGGHWPFGWFLCKFTFTIVDINLFGSVFLIALIA 120  
QY 121 LDRICVLHPVWQNHRTVSLAMRVIVGVPWTLALVLTLPVLELFTTTPNGDYCTFNF 180  
Db 121 LDRVCVLHPVWQNHRTVSLAMRVIVGVPWTLALVLTLPVLELFTTTPNGDYCTFNF 180  
QY 181 ASWGTPERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAAKHKKMKSSRPL 240  
Db 181 SPWTNDPKRINAVAMLTGRIIRFVIGFSLPMSIVAICYGLIAAKHKKMKSSRPL 240  
QY 241 RVLTAVASFFICWFPQVALLGTVLWVKEMLFYKGYKIIDILVNPSSLAFFNSCLNPM 300  
Db 241 RVLSEFAAFAFFLWSPQVALLGTVLWVKEMLFYKGYKIIDILVNPSSLAFFNSCLNPM 300  
QY 301 LYVFGQDFRERLHSLTSLERALSSEDSAPTNDTAANSAPPAETELQA 350  
Db 300 LYVFGQDFRERLHSLTSLERALSSEDSAPTNDTAANSAPPAETELQA 350

RESULT 4  
AAO21656  
ID AAO21656 standard; Protein; 343 AA.

XX AAO21656;  
XX 05-SEP-2002 (first entry)  
XX Mouse protein homologous to Mus musculus FMRL-3 protein.  
XX Antibacterial; fungicide; protozoacide; virucide; anti-HIV; analgesic;  
KW cytostatic; diabetes; anorectic; anabolic; antiasthmatic; cardiovascular;  
KW antiparkinsonian; hypotensive; hypertensive; renal; antitumor; relaxant;  
KW osteopathic; antiangiinal; antiischemic; antiallergic; antimigraine;  
KW antiemetic; neuroprotective; tranquiliser; antischizophrenic; nootropic;  
KW antidepressant; anticonvulsant; FMRL-3v; FMRL-3; HIV-1; HIV-2; pain;  
KW cancer; diabetes; obesity; anorexia; bulimia; asthma; urinary retention;  
KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
KW osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;  
KW allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic;  
KW neurological disorder; anxiety; schizophrenia; manic depression;  
KW delirium; dementia; severe mental retardation; dyskinesias; gene therapy;  
KW Huntington's disease; Gilles de la Tourette's syndrome; protein therapy;  
KW vaccine; mouse; murine.  
XX Mus musculus.  
XX OS  
XX US2002045216-A1.  
XX 18-APR-2002.  
XX 12-JUN-2001; 2001US-0879017.  
XX 12-JUN-2000; 2000US-210944P.  
XX (ELSH/) ELSHOURBAGY N.  
XX (LANE/) LANE P.  
XX (TSUI/) TSUI P.  
XX Eishourbagy N, Lane P, Tsui P;  
XX WPI; 2002-507239/54.  
XX N-PSDB; AAL39617.  
XX Isolated polynucleotides encoding Mus Musculus FMRL-3v, useful for  
PT identifying compounds for treating e.g. cancers, Parkinson's diseases  
PT and depression -  
XX Claim 4; Page 13; 16pp; English.  
XX The invention relates to isolated polynucleotides encoding Mus Musculus  
CC FMRL-3v proteins. The M. Musculus FMRL-3 polynucleotides and their vector  
CC may be used in a process for producing the FMRL-3 polypeptides by  
CC recombinant techniques in a host cell. The FMRL-3 polypeptides may be  
CC used in assays for screening for compounds that either agonise or  
CC antagonise M. Musculus FMRL-3. The compounds identified are useful in  
CC the treatment of human diseases e.g. infections such as bacterial, in  
CC fungal, protozoan and viral infections (particularly infections by Human  
CC immunodeficiency Virus (HIV)-1 or HIV-2), pain, cancers, diabetes,  
CC obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart  
CC failure, hypotension, hypertension, urinary retention, osteoporosis,  
CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign  
CC prostatic hypertrophy; migraine, vomiting, psychotic and neurological  
CC disorders (including anxiety, schizophrenia, manic depression,  
CC depression, delirium, dementia, and severe mental retardation) and  
CC dyskinesias (such as Huntington's disease or Gilles de la Tourette's  
CC syndrome). The polynucleotides and proteins of the invention can be used  
CC in the treatment of disorders by gene therapy, protein therapy and  
CC vaccination. This sequence represents a mouse protein with homology to  
CC the Mus musculus FMRL-3 protein of the invention.  
XX  
XX Sequence 343 AA;

Query Match 63.7%; Score 1157.5; DB 23; Length 343;  
Best Local Similarity 65.8%; Pred. No. 1.7e-121;  
Matches 229; Conservative 39; Mismatches 75; Indels 5; Gaps 1;

QY 1 METNESTPLNEEVEYSAGYTVLRILPLVLGVTVFVLGNGLVIVWAGFRMTVT 60  
 DB 1 MEANSIPLNGSEVFFYDSTTSRVLWILSVIVLSITFVLGNGLVIVWAGFRMAHTVT 60  
 QY 61 TTYCINLALADESFATLPFLIVSAMGKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
 DB 61 TTYCINLALGDSFVWTLPLHIISWMGKWLFGFLCKFVLSIVHINLFSVFLITLIA 120  
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIIVGFWILALVLTLPVFLFVLTTPNGDITCTNF 180  
 DB 121 MDRCTCVLPVWQAQNHRTVSLAMKVIIVGFWILALVLTLPVFLFVLTTPNGDITCTNF 180  
 QY 181 ASWGGTPEERLVAITMLTARGIIRVIGFSLPMSIVACYGLIAAKHKKMIKSSRPL 240  
 DB 181 ESWVAPNEQLKVSITVSTATGIISFIIGFSLPMSFVACYGLIAAKICRKGFLSSRPL 240  
 QY 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKIKIIDLNVPTSSLAFFNSCLNPM 300  
 DB 241 RVLTVAVASFFICWPFQVALLGVWVKEMLFYKIKIIDLNVPTSSLAFFNSCLNPM 300  
 QY 301 LVYFGQDPRKLIHSLPFLSRLSEDSAPTNDTAANSASPPAETEL 348  
 DB 296 LVYFLGQEPREKLIYSLSSLERALREDSVLSGKSSNFSSCPADSEL 343

RESULT 5  
 AAR48713  
 ID AAR48713 standard; Protein; 315 AA.  
 AC AAR48713;  
 XX AAR48713;  
 DT 06-JUN-1996 (first entry)  
 DE G-protein coupled human N-formyl peptide receptor protein.  
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;  
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;  
 KW rhodopsin; opsin; odorant; cytomagalovirus.  
 OS Homo sapiens.  
 PN W09405695-A1.  
 PD 17-MAR-1994.  
 XX 09-SEP-1993; 93WO-US08528.  
 XX 10-SEP-1992; 92US-0943236.  
 PA (UYNV ) UNIV NEW YORK STATE.  
 PI Murphy RB, Schuster DI;  
 DR WPI; 1994-101120/12.  
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for  
 PT binding GPR ligands or modulating GPR binding  
 PS Disclosure; Page 87-88; 160pp; English.  
 CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor  
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,  
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,  
 CC odorant, cytomagalovirus and other G-protein coupled receptors. The  
 CC receptor proteins were used to design polypeptides, pref. based on the  
 CC transmembrane domains, for use in G-protein coupled receptor ligand  
 CC binding assays. The polypeptide fragments retain biological activity  
 CC such as binding a GPR ligand or modulating GPR binding to a GPR  
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples  
 CC of polypeptide fragments). The polypeptide fragments can be used in  
 CC compositions for treating subjects suffering from a pathology related to

CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.  
 XX Sequence 315 AA;  
 SQ Query Match 61.5%; Score 1117; DB 15; Length 315;  
 Best Local Similarity 67.3%; Pred. No. 5.5e-117;  
 Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;  
 QY 27 TLPLVLGVTVFVLGNGLVIVWAGFRMTVTTCYINLALADESFATLPFLIVSMA 86  
 DB 1 ITTILVFAVRFLVGLVGLNGLVIVWAGFRMTVTTCYINLALADESFATLPFLIVSMA 60  
 QY 87 MGEKPPGFWFLCKLIHIVVDINLFGSVFLIGFIALDRICVLPVWQAQNHRTVSLAMKVI 146  
 DB 61 ---HWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRICVLPVWQAQNHRTVSLAMKVI 117  
 QY 147 VGPWTALVLTLPVFLFVLTTPNGDITCTNFASWGGTPEERLVAITMLTARGIIRF 206  
 DB 118 IGPWYVALLVLPVIRVITVPGKGTGTVACFTNFPNDPKERINAVAMLTVRGIIRF 177  
 QY 207 VIGFSLPMSIVACYGLIAAKHKKMIKSSRPLRVLTAVVASFFICWPFQVALLGTV 266  
 DB 178 IIGFSAPIVAVSYGLIATKI-----IKSSRPLRVLSFVAAAFVLCWSYQVVALIATV 232  
 QY 267 WLKEMLFYKIKIIDLNVPTSSLAFFNSCLNPMLYVFGQDPRKLIHSLPFLSRLSALS 326  
 DB 233 RIRELL-QGMYKEIGIADVDTSAIAFFNSCLNP-LYVFGQDPRKLIHSLPFLSRLSALS 290  
 QY 327 EDSAPTNDTAANSASPPAETELQA 350  
 DB 291 EDSTQTSATNSTLPSAEVALQA 314

RESULT 6  
 AAW02685  
 ID AAW02685 standard; peptide; 315 AA.  
 AC AAW02685;  
 XX AAW02685;  
 DT 12-NOV-1996 (first entry)  
 DE G-protein coupled human N-formyl peptide receptor.  
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;  
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;  
 KW odorant; cytomagalovirus; serotonergic.  
 OS Homo sapiens.  
 PN US5508384-A.  
 PD 16-APR-1996.  
 XX 10-SEP-1992; 92US-0943236.  
 XX 09-SEP-1993; 93US-0118270.  
 PR 10-SEP-1992; 92US-0943236.  
 XX (UYNV ) UNIV NEW YORK STATE.  
 PI Murphy RB, Schuster DI;  
 DR WPI; 1996-208785/21.  
 XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.  
 PT for treating schizophrenia  
 XX Disclosure; Column 97-100; 184pp; English.  
 PS Proteins AAW02657-W02730 represent a range of G-protein coupled receptor  
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,  
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,

CC odorant, cytomegaloviral and other GPR proteins. The receptor proteins  
CC domains, for use in G-protein coupled receptor ligand binding assays.  
CC The polypeptide fragments retain biological activity such as binding a  
CC GPR ligand or modulating GPR ligand binding to a GPR (see  
CC AA02747-W02999 for examples of polypeptide fragments). The polypeptide  
CC fragments can be used in compositions for treating subjects suffering  
CC from a pathology related to a GPR abnormality e.g. a psychotic disorder  
CC such as schizophrenia.  
XX  
SQ Sequence 315 AA;

Query Match 61.58; Score 1117; DB 17; Length 315;  
Best Local Similarity 67.38; Pred. No. 5.5e-117;  
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;

Qy 27 ILPLVLGVTPLVGLNGVLVWAGFRMTVTTCYLNALADFSFATLPFLIVSMA 86  
Db 1 IITVLVFAVRFLVGLNGVLVWAGFRMTVTTCYLNALADFSFATLPFLIVSMA 60  
87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLPVWQNHRTVSLAMKVI 146  
Db 61 ---HWPEFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLPVWQNHRTVSLAMKVI 117  
Qy 147 VGPWILALVLPVFLFTVTTPNGDTCYCFNFASGGTPEERLKVAITMLTARGIIRF 206  
Db 118 IGPWVALLLPVIRVTIYVPGTGVACVFNFSPTNDPKERINAVAMLTVRGIIRF 177  
Qy 207 VIGFSLPMSIYAICYGLIAAKIHKMGKIKSRRLRVLTAFAVAFSFFICWFPQVALLGTV 266  
Db 178 IIGFSAFMSIYAVSVGLIATKI-----IKSRRLRVLTAFAVAFSFFICWFPQVALLGTV 232  
Qy 267 WLKEMFLGKTKIIDLNVPTSSLAFFNSCLNPMLYVFGQDFRERLIHSLPTSLEALS 326  
Db 233 RIRELL-QGMYKEIGADVTSATAFFNSCLNP-LYVFMGQDFRERLIHALPASLERALT 290  
Qy 327 EDSAPTNDTAANSAPPAETELQA 350  
Db 291 EDSQTSTATNSTLPSAEVALQA 314

RESULT 7  
AA90678  
ID AA90678 standard; Protein; 356 AA.  
AC AA90678;

DT 21-AUG-2000 (first entry)  
XX Human G protein-coupled receptor GPR32.

XX G protein-coupled receptor; GPCR; constitutively active;  
KW intracellular loop 3; transmembrane domain 6; drug screening;  
KW agonist; antagonist.

OS Homo sapiens.  
XX  
PN WO200022129-A1.  
XX  
PD 20-APR-2000.  
XX  
PF 12-OCT-1999; 99WO-US23938.  
XX  
PR 13-OCT-1998; 98US-0170496.  
XX  
PA (AREN-) ARENA PHARM INC.

PI Behan DP, Chalmers DT, Liaw CW;  
XX  
DR WPT; 2000-329165/28.  
DR N-PSDB; AAA30756.  
XX  
PT Non-endogenous constitutively activated human G protein-coupled

PT receptors, useful for identifying agonists for use as pharmaceutical  
XX agents  
PS  
XX Example 1; Page 305-306; 341pp; English.

CC The invention relates to constitutively active, non-endogenous versions  
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AA90643-  
CC AA90677 and AA90683-190867), and to DNA encoding them (AA30709-A30743  
CC and AA30775-A30779). The mutant proteins of the invention contain a  
CC mutation in a portion of the protein comprising intracellular loop 3  
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,  
CC is substituted for an endogenous residue in IC3 at a position 16 amino  
CC acids N-terminal of an endogenous proline in TM6 to form a sequence  
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg  
CC or Ala, and is preferably Lys. When the endogenous residue at this  
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.  
CC The 15 amino acid stretch between the substituted amino acid and the Pro  
CC may be endogenous, non-endogenous, or a mixture of endogenous and  
CC non-endogenous residues. The constitutively active GPCRs are useful for  
CC identifying antagonists, agonists and partial agonists for use as  
CC pharmaceutical agents. The mutant proteins are also useful in research  
CC settings for elucidating the roles of the receptors in normal and  
CC diseased conditions. Antagonists for a particular GPCR are useful for  
CC treating diseases and disorders associated with that receptor. Because  
CC the novel mutant GPCRs are constitutively active, they can be used  
CC directly for screening of compounds without the need for endogenous  
CC ligands. The present sequence represents a human wild-type GPCR referred  
CC to in an exemplification of the invention.

SQ Sequence 356 AA;

Query Match 30.58; Score 554.5; DB 21; Length 356;  
Best Local Similarity 41.08; Pred. No. 1.4e-53;  
Matches 126; Conservative 59; Mismatches 113; Indels 9; Gaps 4;

Qy 25 LRILPLVVLGVTFLVGLNGVLVWAGFRMTVTTCYLNALADFSFATLP---FL 81  
Db 42 LRPLTVVILSASIVVGLNGVLVWAGFRMTVTTCYLNALADFSFATLPDIAMYY 101  
Qy 82 IVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLPVWQNHRTVSL 141  
Db 102 IVS----ROWLGEWACKLYITFVFLSYFASNCLLVFISVDRICISVLPVWALNHRVTQR 157  
Qy 142 AMKVIVGFWIILALVLPVFLFTVTTPNGDTCYCFNFASGGTPEERLKVAITMLTAR 201  
Db 158 ASWLAFGVWLLAALCSAHLKERTRKW-NGCTCYLAFNSDNETAQIWEGVVEGHIIG 216  
Qy 202 GIIRFVIGFSLPMSIYAICYGLIAAKIHKMGKIKSRRLRVLTAFAVAFSFFICWFPQV 261  
Db 217 TIGHFLGFLGLAIGTCAHLIRAKLIREGVWVHARRPARLLLVLSAFFIFWSPFNVV- 275  
Qy 262 LLGTVWLKEMFLYGKTKIIDLNVPTSSLAFFNSCLNPMLYVFGQDFRERLIHSLPTS 321  
Db 276 LLVHLRRVRLKEIYHPRMLLILQASFALGVNSNLPFLYVFGDRGFQERFQSLTSAL 335  
Qy 322 ERAISED 328  
Db 336 ARAFGE 342

RESULT 8  
AA90683  
ID AA90683 standard; Protein; 356 AA.  
XX  
AC AA90683;

DT 21-AUG-2000 (first entry)  
XX Human mutant G protein-coupled receptor GPR32 (K255A).

XX G protein-coupled receptor; GPCR; constitutively active;  
KW intracellular loop 3; transmembrane domain 6; drug screening;  
KW agonist; antagonist; mutant; mutein.



Db 144 GCVWVAFVVCVFPVY-RDLFMDNRSICRYNFDSSRSYDWDYVYKLSLPESNSTNS 202  
 Qy 183 -----WGGTPEE 189  
 Db 203 TAQLTGHNDRSAPSSVQARDYFWVTVALQSOPFLTSPEDSFLDSANQOPHYGKPPN 262  
 Qy 190 RLKVAI-----195  
 Db 263 VLTAAVSGFPVEDRKSNTLNADAFLSAHTLFTPTASSGHLYPYDQGDYVDQFTYDNHV 322  
 Qy 196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGMIKS-SRPLRLVLTAVVASFFIC 253  
 Db 323 PTPLMAITITRLVGVGLVFPFFIWCYSLIVFRMKTFTKSRNKTFRVAVAVVTVFFIC 382  
 Qy 254 WFPFQVALLGTWVLKEMLFYGYKIIDLIVNPTSS-----LAFFNSCLNP 299  
 Db 383 WTPYHLVG-----VLLITDPESLGEAVMSWDHMSIALASANSFCNP 425  
 Qy 300 MLYVFGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAS 341  
 Db 426 FLYALLGDKFRKKARQSIKGIIEAFAFSEELTHSTNCTQDKAS 467  
 RESULT 10  
 AAU75166  
 ID AAU75166 standard; Protein; 477 AA.  
 AC AAU75166;  
 DT 08-MAY-2002 (first entry)  
 DE Mouse anaphylatoxin C3a receptor.  
 KW Mouse; transgenic; disruption of target gene; disease model;  
 KW modulation of gene expression; behavioural phenotype; thymus abnormality;  
 KW seizure; stimulus processing; anaphylatoxin C3a receptor; receptor.  
 OS Mus musculus.  
 XX WO200201950-A2.  
 XX 10-JAN-2002.  
 XX 29-JUN-2001; 2001WO-US20795.  
 XX 29-JUN-2000; 2000US-215178P.  
 XX 29-JUN-2000; 2000US-215179P.  
 XX 29-JUN-2000; 2000US-215366P.  
 XX 29-JUN-2000; 2000US-215402P.  
 XX 29-JUN-2000; 2000US-215404P.  
 XX 29-JUN-2000; 2000US-215466P.  
 XX 27-JUL-2000; 2000US-215467P.  
 XX 26-OCT-2000; 2000US-244083P.  
 XX (DELT-) DELTAGEN INC.  
 XX Leviten MW, Brennan TJ, Guenther C, Klein R, Matthews W, Moore M;  
 WPI: 2002-164479/21.  
 DR N-FSDB; ABK13745.  
 XX Novel transgenic mouse comprising disruption in target gene e.g., an  
 PT anaphylatoxin C3a receptor gene, chordin gene, useful for identifying  
 FT agents that modulate expression or function of target gene  
 XX Disclosure; Fig 1; 90pp; English.  
 XX The present invention relates to a method of creating transgenic animals,  
 CC particularly transgenic mice, comprising a disruption in a target gene.  
 CC Examples of target genes given in the specification include the mouse  
 CC anaphylatoxin C3a receptor gene, 5-HT5A gene, chordin gene, RORgamma

CC gene, BMP gene, airway trypsin-like protease gene and the aquaporin  
 CC gene. The transgenic mice are useful as models for disease and for  
 CC identifying an agent that modulates the expression or function of a  
 CC gene. The transgenic mice models are useful for identifying drugs and  
 CC pharmaceutical therapies. They are also useful for testing and developing  
 CC new treatments relating to behavioural phenotypes. They are useful for  
 CC potential treatments for various diseases. For example, a transgenic  
 CC mouse comprising a disruption in the anaphylatoxin C3a receptor gene is  
 CC useful for identifying an agent that ameliorates a thymus abnormality,  
 CC an increased susceptibility to seizure, or a stimulus processing deficit.  
 CC The present sequence represents mouse anaphylatoxin C3a receptor. The  
 CC encoding gene is disrupted to produce transgenic mice in the methods  
 CC of the present invention.  
 XX SQ Sequence 477 AA;  
 Query Match 29.9%; Score 542.5; DB 23; Length 477;  
 Best Local Similarity 28.1%; Pred. No. 4.8e-52;  
 Matches 130; Conservative 58; Mismatches 109; Indels 165; Gaps 6;  
 Qy 27 ILPLVVLGVTFVLGVLGNGLVIVAGFRMTRVTTTCYLNALADFSFTATPLFLIVSMA 86  
 Db 24 IASVMTLGLTCLLGLGNGLVWAGVKMKTTVNTWFLHLTLADFLCCLSLPFSLAHLI 83  
 Qy 87 MGEKWPFGWFLCKLHIIVVDINLFGSVFLIGFALDRCICVLPWQAHNRVSLAMKYI 146  
 Db 84 LQGHWPYGLFLCKLIPSIILNMFASVFLTLAISDRCLIVHKPIWQCNHRNVRTAFAIC 143  
 Qy 147 VGPWILALVLTLPVFLFTVTTPNGDTYCTENFAS-----182  
 Db 144 GCVWVAFVVCVFPVY-RDLFMDNRSICRYNFDSSRSYDWDYVYKLSLPESNSTNS 202  
 Qy 183 -----WGGTPEE 189  
 Db 203 TAQLTGHNDRSAPSSVQARDYFWVTVALQSOPFLTSPEDSFLDSANQOPHYGKPPN 262  
 Qy 190 RLKVAI-----195  
 Db 263 VLTAAVSGFPVEDRKSNTLNADAFLSAHTLFTPTASSGHLYPYDQGDYVDQFTYDNHV 322  
 Qy 196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGMIKS-SRPLRLVLTAVVASFFIC 253  
 Db 323 PTPLMAITITRLVGVGLVFPFFIWCYSLIVFRMKTFTKSRNKTFRVAVAVVTVFFIC 382  
 Qy 254 WFPFQVALLGTWVLKEMLFYGYKIIDLIVNPTSS-----LAFFNSCLNP 299  
 Db 383 WTPYHLVG-----VLLITDPESLGEAVMSWDHMSIALASANSFCNP 425  
 Qy 300 MLYVFGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAS 341  
 Db 426 FLYALLGDKFRKKARQSIKGIIEAFAFSEELTHSTNCTQDKAS 467  
 RESULT 11  
 AAU86323  
 ID AAU86323 standard; Protein; 372 AA.  
 AC AAU86323;  
 DT 01-MAR-1999 (first entry)  
 DE Kidney injury associated molecule HW055 protein.  
 XX Kidney injury associated molecule; kidney injury related molecule;  
 KW KIM; tissue growth promotion; regeneration; renal condition;  
 KW acute renal failure; acute nephritis; tumour.  
 XX Rattus sp.  
 XX WO9853071-A1.  
 XX 26-NOV-1998.  
 XX

PF 22-MAY-1998; 98WO-US10547.  
XX 23-MAY-1997; 97US-0047491.  
PR 23-MAY-1997; 97US-0047490.  
XX (BIOJ ) BIOGEN INC.  
XX Cate RL, Hession CA, Sanicola-Nadel M, Wei H;  
PI WPI; 1999-045312/04.  
XX N-PSDB; AAV80608.  
DR Kidney injury-associated molecule, KIM, polypeptides - upregulated  
XX in injured or regenerating tissues, useful to promote tissue growth  
XX and regeneration, especially to treat renal conditions  
XX  
XX Claim 17; Page 125-126; 213pp; English.  
XX  
XX The present sequence represents a kidney injury associated molecule  
XX (KIM) protein. KIM proteins can be administered therapeutically  
XX by expressing KIM encoding polynucleotides, to promote growth and/or  
XX survival of damaged tissue (e.g. renal tissue), since the KIM proteins  
XX are upregulated in injured or regenerating (especially renal) tissues.  
XX KIM fusion proteins, conjugates, antibodies and vectors can also be used  
XX therapeutically, e.g. these or the KIM proteins may be included with an  
XX acceptable carrier in pharmaceutical compositions, useful for therapy/  
XX prophylaxis of conditions associated with dysfunction/disregulation of  
XX KIM genes or proteins, especially renal diseases or impairments of renal  
XX function in humans (e.g. acute renal failure, acute nephritis). The  
XX polynucleotides can be used to produce antisense sequences which, when  
XX internalised into cells, can disrupt expression of a cellular KIM gene,  
XX also useful in therapy (e.g. to block the growth of tumours dependent on  
XX KIM for growth) or compositions. The proteins and polynucleotides are  
XX useful diagnostically e.g. to detect and quantify renal injury/disease  
XX (indicative of increased risk, or presence of, renal injury or impaired  
XX function), or abnormal responses to tissue injury (indicative of  
XX increased risk, or presence of, an autoimmune response or abnormal  
XX tissue growth arising from/affecting renal tissue). The proteins can  
XX also be used to locate KIM-producing cells (especially specific loci,  
XX e.g. tissue masses abnormally producing/expressing KIM such as tumours  
XX arising from/affecting renal tissue), by contacting cells with an  
XX imageable KIM-binding reagent and imaging reagent accumulation.  
XX  
XX Sequence 372 AA;  
SQ  
Query Match 29.8%; Score 542; DB 20; Length 372;  
Best Local Similarity 35.5%; Pred. No. 3.9e-52;  
Matches 123; Conservative 66; Mismatches 119; Indels 38; Gaps 8;  
11 EYEE-----VYESAG---YTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRVTVTI 62  
15 EYSDGSDYIVDLEAGPLEAKVAEFLVVIYSLVCFGLGILGNGLVIVATFRMKTNTV 74  
63 CYLNALADFSFATLPEFLIVSMANCEKWPFCWFLCKLHIVVDNLFCSVFLGFIADL 122  
75 WFNVLAVADFLNFIPLIHITTAAMDYHWVFGKAMCKISSFLSHNMVYSVFLLVISPD 134  
123 RCICVLHPVWQNHRTSVSLAMKVIIVGPIWILALVTLPLVFLFTTVPNGDYCYCFNFAS 182  
135 RCISVLLPWQSNHRSVRSLAYWTCVWVWVLAFLSPSLVFRDVTSTSGKITCFNNFSL 194  
183 WGGTPEE-----RLKVAITMLTARGIIRFVIGFSLPMSVIAICYIAUKI 228  
195 ---AAPEPESHSTHPTDPVGYSRHVAVT-----VTRFLCGFLPIPVFIITACVLTIVFKL 246  
229 HKGGMKSRRLVLTAVVASFCWFFPOLVALLGTWVKEMLYGKYKIIDLVPNT 287  
247 QNRRLAKTKPKKPIITITITIFLCPCPH-----TYLLELHHTVAPSVFSLGLPIA 300  
288 SSLAFNNSCLNMLYVFVGQDFRERLIHSLPTSLERALSSEDAPT 333  
301 TAVATANSNMNPILYVFMCHDFKFKV-ALFSRLYNALSEDGPPSS 345

RESULT 12  
AAW23367  
ID AAW23367 standard; Protein; 482 AA.  
XX  
XX AAW23367;  
AC AAW23367;  
XX  
XX 30-MAR-1998 (first entry)  
XX  
XX Novel G-protein coupled receptor with an enlarged extracellular domain.  
XX  
XX G-protein coupled receptor; enlarged extracellular loop;  
XX inflammatory disease; asthma; chronic obstructive pulmonary disease;  
XX cystic fibrosis; multiple sclerosis; antibody.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX Modified-site 9  
XX Domain /note= "predicted N-glycosylation site"  
XX 22..160  
XX Domain /note= "putative transmembrane domain"  
XX 163..327  
XX Domain /note= "enlarged extracellular loop"  
XX 194  
XX Modified-site  
XX /note= "predicted N-glycosylation site"  
XX 333..439  
XX Domain /note= "putative transmembrane domain"  
XX  
XX WO9728188-A1.  
XX  
XX 07-AUG-1997.  
XX  
XX 30-JAN-1997; 97WO-US01736.  
XX  
XX 30-JAN-1996; 96US-0010808.  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Ye RD;  
XX  
XX WPI; 1997-402552/37.  
XX N-PSDB; AAT64946.  
XX  
XX G-protein-coupled receptor with enlarged extracellular domain -  
XX between fourth and fifth transmembrane domains, also nucleic acid  
XX and antibodies useful for treating inflammation and neurological  
XX disease  
XX  
XX Claim 4; Fig 1; 54pp; English.  
XX  
XX The present sequence represents a novel G-protein coupled receptor  
XX that has an enlarged extracellular loop between the fourth and fifth  
XX transmembrane domains. Antibodies generated against the present  
XX protein revealed expression in a variety of tissues, including  
XX heart, lung and placenta. Diseases or conditions mediated by the  
XX G-protein coupled receptor can be treated by administering reagents such  
XX as the present sequence, antisense nucleic acid or antibodies generated  
XX against the receptor. Reagents may comprise a molecule binding to the  
XX receptor but not transmitting a signal across the cell membrane or  
XX reducing effectiveness of binding of the natural ligand. The reagent may  
XX also alter the interaction of the receptor with the G-protein with which  
XX it naturally reacts e.g. by altering phosphorylation sites in  
XX intracellular domains of the receptor. Inflammatory diseases or  
XX conditions mediated by the novel receptor which can be treated include  
XX e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis,  
XX multiple sclerosis. The antibody can also be used to diagnose these  
XX diseases e.g. in brain tissue from patients with suspected neurological  
XX disease, especially Alzheimer's, in skin samples especially from patients  
XX with a suspected inflammatory disease or in haematopoietic cells. The  
XX nucleic acids are also useful in screening for compounds modulating gene  
XX expression by standard assays.



SQ Sequence 482 AA;

Query Match 28.0%; Score 509.5; DB 18; Length 482;  
 Best Local Similarity 26.6%; Pred. No. 2.5e-48;  
 Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN----FSTPLNEYEEVSYESAGYTVLRILPLVLGVGTVFVLGVNGLVWAGFRMTR 57  
 DB 7 ETNSTDLLSQPNNEPPV-----ILSMVILSLTFLGPGNGLVWAGLKMQR 54

QY 58 TVTTCYLNALADESFATLPLFLIVSMAMGEKWPFGFLCKLIHVVDINLFGSVFLIG 117  
 DB 55 TVNTIWFHLTLADLLCLSLPFSLAHLAQGWPGYREFLCKLIPSIIVLNMFAVFLLT 114

QY 118 FIALDRICVLHPVWQAHNRHTVSLAMKVIWGPWILALVLPFLFTVTIPNGDYCT 177  
 DB 115 AISLDRCLVFKPIWQNHNRVGMACSGCIWVAVFVVCIPVYRIEFTDHNHR-CG 173

QY 178 FNFA-----SW-----183  
 DB 174 YKFGLSLLDYPDFYGDPLENRSLENIQVRGEMNDRLDPSFTNDHPWTVPTVFQPT 233

QY 184 -----GGTPEE-----190  
 DB 234 FQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPSGFPEDHETSPLDNSDAFLSTH 293

QY 191 LKV-----ATMLTARGIIRFVIGFSLPMSIVA 218  
 DB 294 LKLFPSSASSNFYSELPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLLEFSVIMI 353

QY 219 ICYGLIAAKIHKGMKIS-SRPLRLVLTAVASFFTCWFPFVALLGTVWVKEMLFYQKY 277  
 DB 354 ACYSFIVFMQGRGFAKSQSKTFRVAVVVAVFLVCWTPYHI-----F 396

QY 278 KIIDLNVNPTS-----SLAFFNSCLNPMLYVFGQDFRERLIHSLPTSILR 323  
 DB 397 GVLSLLDTPETPLGKTLMSWDHVCIALASANSFCNPFYALLGDKFRKARQSIQIGILEA 456

QY 324 ALSKD-----SAPNDTAANSAS 341  
 DB 457 AFSEELRSTRCHPSNNVISERN 479

RESULT 13  
 AAW42376  
 ID AAW42376 standard; Protein; 482 AA.  
 AC AAW42376;  
 XX 08-JUN-1998 (first entry)  
 XX Homo sapiens C3a receptor.  
 XX C3a receptor; treatment; diagnosis; atherosclerosis; chronic;  
 KW polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's;  
 KW disease; acute inflammatory disease; Crohn's disease; food;  
 KW allergies; non-bronchial allergies; osteoarthritis; osteoporosis;  
 KW thyroid disease; coronary heart disease.  
 XX Homo sapiens.  
 XX EP814158-A2.  
 XX 29-DEC-1997.  
 XX 17-JUN-1997; 97EP-0304250.  
 XX 17-JUN-1996; 96US-0019627.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX Ames RS, Bergsma DJ, Foley JJ, Kumar C, Sarau HM;

DR WPI: 1998-044336/05.  
 XX N-PSDB; AAV03250.  
 PT C3a receptor agonists, antibodies and antagonists - useful for  
 PT diagnosis of disease related to expression of C3a receptor, e.g.  
 PT acute inflammatory disease, atherosclerosis, chronic polyarthritis,  
 PT etc.  
 XX Disclosure; Fig 1; 43pp; English.  
 XX The sequence is that of the C3a receptor. It can be used in a process  
 CC for diagnosing a disease or susceptibility to a disease related to  
 CC expression of the C3a receptor. This process involves analysing for  
 CC the presence of a the C3a receptor in a sample derived from a patient  
 CC suspected of having such a disease. C3a receptor-related diseases that  
 CC can be detected by this method comprise acute inflammatory disease,  
 CC atherosclerosis, chronic polyarthritis, systemic vasculitis, multiple  
 CC sclerosis, Alzheimer's Disease, CNS inflammatory disease, Crohn's  
 CC Disease, food allergies, non-bronchial allergies, osteoarthritis,  
 CC osteoporosis, thyroid disease, coronary heart disease, Systemic Lupus  
 CC Erythematosus SLE-associated nephritis, membranoproliferative GN,  
 CC membranous nephritis, rheumatoid arthritis, Behcet's syndrome, juvenile  
 CC rheumatoid arthritis, Sjogren's syndrome, myasthenia gravis, cerebral  
 CC lupus, Guillain-Barre syndrome, pemphigus/pemphigoid, phototoxic  
 CC reactions, vasculitis, post-bypass syndrome, catheter reactions, sepsis,  
 CC ARDS, anaphylaxis, transplant rejection, pre-eclampsia, atheroma, bowel  
 CC inflammation, thyroiditis, infertility, susceptibility to pyogenic  
 CC infections, glomerulonephritis, susceptibility to neisserial infections,  
 CC recurrent subcutaneous swelling and mucosal oedema, and recurrent  
 CC episodes of thrombosis/haemolysis. C3a receptor agonists, antagonists  
 CC and antibodies can be used in the treatment of patients having need to  
 CC inhibit or activate a C3a receptor.  
 XX SQ Sequence 482 AA;  
 Query Match 28.0%; Score 509.5; DB 19; Length 482;  
 Best Local Similarity 26.6%; Pred. No. 2.5e-48;  
 Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN----FSTPLNEYEEVSYESAGYTVLRILPLVLGVGTVFVLGVNGLVWAGFRMTR 57  
 DB 7 ETNSTDLLSQPNNEPPV-----ILSMVILSLTFLGPGNGLVWAGLKMQR 54

QY 58 TVTTCYLNALADESFATLPLFLIVSMAMGEKWPFGFLCKLIHVVDINLFGSVFLIG 117  
 DB 55 TVNTIWFHLTLADLLCLSLPFSLAHLAQGWPGYREFLCKLIPSIIVLNMFAVFLLT 114

QY 118 FIALDRICVLHPVWQAHNRHTVSLAMKVIWGPWILALVLPFLFTVTIPNGDYCT 177  
 DB 115 AISLDRCLVFKPIWQNHNRVGMACSGCIWVAVFVVCIPVYRIEFTDHNHR-CG 173

QY 178 FNFA-----SW-----183  
 DB 174 YKFGLSLLDYPDFYGDPLENRSLENIQVRGEMNDRLDPSFTNDHPWTVPTVFQPT 233

QY 184 -----GGTPEE-----190  
 DB 234 FQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPSGFPEDHETSPLDNSDAFLSTH 293

QY 191 LKV-----ATMLTARGIIRFVIGFSLPMSIVA 218  
 DB 294 LKLFPSSASSNFYSELPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLLEFSVIMI 353

QY 219 ICYGLIAAKIHKGMKIS-SRPLRLVLTAVASFFTCWFPFVALLGTVWVKEMLFYQKY 277  
 DB 354 ACYSFIVFMQGRGFAKSQSKTFRVAVVVAVFLVCWTPYHI-----F 396

QY 278 KIIDLNVNPTS-----SLAFFNSCLNPMLYVFGQDFRERLIHSLPTSILR 323  
 DB 397 GVLSLLDTPETPLGKTLMSWDHVCIALASANSFCNPFYALLGDKFRKARQSIQIGILEA 456

QY 324 ALSKD-----SAPNDTAANSAS 341  
 DB 457 AFSEELRSTRCHPSNNVISERN 479





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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:17:27 : Search time 20 Seconds  
(without alignments)  
1687.159 Million cell updates/sec

Title: US-09-944-807-2  
Perfect score: 1817  
Sequence: 1 MEINFSPLENEYEVSYESA.....TNDTAANSASPPATELQAM 351

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	2 B42009	FMLP-related recep
2	1318	72.5	353	2 C42009	FMLP-related recep
3	1249.5	68.8	350	2 A42009	N-formyl peptide r
4	1223.5	67.3	352	2 A46520	N-formyl peptide r
5	1174.5	64.6	364	2 A49542	N-formyl peptide c
6	538.5	29.6	371	2 JC5498	G protein-coupled
7	530.5	29.2	473	2 JC5835	anaphylatoxin C3a
8	513	28.2	350	1 A37963	complement C5a ana
9	509.5	28.0	482	2 S65766	G protein-coupled
10	502.5	27.7	371	2 JC5796	probable chemoattr
11	502	27.6	353	2 JC2492	G protein-coupled
12	500	27.5	352	1 S27357	complement C5a ana
13	499	27.5	355	2 A57533	G protein-coupled
14	457.5	25.2	351	1 A46525	complement C5a ana
15	430.5	23.7	359	2 JC2134	angiotensin II rec
16	427.5	23.5	359	2 JH0621	angiotensin II rec
17	426.5	23.5	359	2 JC1104	angiotensin II rec
18	426.5	23.5	360	2 A53611	interleukin-8 rece
19	423.5	23.3	359	2 S15403	angiotensin II rec
20	422.5	23.3	355	2 JQ1231	interleukin-8 rece
21	420.5	23.1	359	2 A42656	angiotensin II rec
22	420.5	23.1	359	2 JQ1516	angiotensin II rec
23	419.5	23.1	352	2 A45747	neuropeptide Y/pep
24	418.5	23.0	359	2 A48857	angiotensin II rec
25	418.5	23.0	359	2 I39418	angiotensin II rec
26	418	23.0	359	2 S44425	angiotensin II rec
27	413.5	22.8	352	2 G00048	fusin (LESTRA) - c
28	413.5	22.8	359	2 JC1194	angiotensin II rec
29	412	22.7	362	2 A30341	G protein-coupled

30	411.5	22.6	353	2 S28787	neuropeptide Y/pep
31	411.5	22.6	362	2 JN0694	angiotensin II rec
32	405.5	22.3	359	2 I51372	angiotensin II rec
33	405	22.3	418	2 A46226	somatostatin recep
34	403	22.2	359	2 A48921	interleukin-8 rece
35	402	22.1	398	2 I56517	mu opioid receptor
36	402	22.1	428	2 S30508	probable G protein
37	401	22.1	356	2 S42096	interleukin-8 rece
38	401	22.1	358	2 A53752	interleukin-8 rece
39	401	22.1	398	2 A57510	mu opioid receptor
40	399.5	22.0	350	2 A39445	interleukin-8 rece
41	399.5	22.0	391	2 A41795	somatostatin recep
42	399.5	22.0	391	2 C41795	somatostatin recep
43	399.5	22.0	391	2 A39297	somatostatin recep
44	397	21.8	398	2 I56504	mu opioid receptor
45	396	21.8	392	2 S65693	opioid receptor mu

ALIGNMENTS

RESULT 1

B42009

FMLP-related receptor 1 - human

N:Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probab

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 14-Jul-1995 #text\_change 21-Jul-2000

C:Accession: B42009; JCI1258; JQ1521; A42492; I54751; S21581

R:Ba0, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR

A:Reference number: A42009; MUID:92307681; PMID:1612600

A:Accession: B42009

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-263 'A', 265-338, 'C', 340-351 <BAO>

A:Cross-references: GB:M76672

A:Note: authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 a

R:Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.

Gene 118, 303-304, 1992

A:Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor

A:Reference number: JCI1258; MUID:92380523; PMID:1511907

A:Accession: JCI1258

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-351 <PER>

A:Cross-references: EMBL:X63819; NID:g31460; PID:g31461

A:Experimental source: bone marrow mRNA

R:Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochran, C.G.

Biochem. Biophys. Res. Commun. 184, 582-589, 1992

A:Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide recept

A:Reference number: JQ1521; MUID:92246937; PMID:1374236

A:Accession: JQ1521

A:Molecule type: mRNA

A:Residues: 1-351 <YE>

A:Cross-references: GB:M88107; NID:g189862; PID:g189863

A:Experimental source: granulocytes

A:Note: formyl peptide-stimulated calcium mobilization comparable to that of the form

R:Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U.

J. Biol. Chem. 267, 7637-7643, 1992

A:Title: A structural homologue of the N-formyl peptide receptor. Characterization an

A:Reference number: A42492; MUID:92218423; PMID:1373134

A:Accession: A42492

A:Molecule type: mRNA

A:Residues: 1-351 <MUR>

A:Cross-references: GB:M84562; NID:g182741; PIDN:AAA52473.1; PID:g182742

A:Note: sequence extracted from NCBI backbone (NCBIN:94159, NCBIP:94160)

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c

A:Reference number: I54751; MUID:94092629; PMID:7505609

A:Accession: I54751

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-351 <RES>  
A:Cross-references: GB:D10922; NID:g219864; PIDN:BA01720.1; PID:g219865  
C:Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor differentiated myeloid cells and is probably a chemotactic receptor for some other ligand  
C:Genetics:  
A:Gene: GDB:FPRL1  
A:Cross-references: GDB:127554; OMIM:136538  
A:Map position: 19q13.3-19q13.4  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein  
F:27-53/Domain: transmembrane #status predicted <TM>  
F:59-83/Domain: transmembrane #status predicted <TM>  
F:100-121/Domain: transmembrane #status predicted <TM3>  
F:145-169/Domain: transmembrane #status predicted <TM4>  
F:206-226/Domain: transmembrane #status predicted <TM5>  
F:242-266/Domain: transmembrane #status predicted <TM6>  
F:282-307/Domain: transmembrane #status predicted <TM7>  
F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:98-176/Disulfide bonds: #status predicted  
Query Match 100.0%; Score 1817; DB 2: Length 351;  
Best Local Similarity 100.0%; Pred. No. 3.3e-145;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIWVAGFRMTRVT 60  
DB 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIWVAGFRMTRVT 60  
QY 61 TICYLNALADESFATLPFLIVSMAGKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TICYLNALADESFATLPFLIVSMAGKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGWPILALVLTLPVFLFTVTTPNGDTCYTFNF 180  
DB 121 LDRICVLPVWQAQNHRTVSLAMKVIVGWPILALVLTLPVFLFTVTTPNGDTCYTFNF 180  
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
QY 241 RVLTVAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTVAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300  
QY 301 LVVFGQDPRERLIHSLPTSLERALS--DSAPTNDTAANSASPPAETELQAM 351  
DB 301 LVVFGQDPRERLIHSLPTSLERALS--DSAPTNDTAANSASPPAETELQAM 351  
RESULT 2  
C42009  
FMLP-related receptor 2 - human  
N:Alternate names: FMLP-related  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 26-Aug-1999  
C:Accession: C42009  
R:Baou, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.  
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), Genomics 13, 437-440, 1992  
A:Reference number: A42009; MUID:92307681; PMID:1612600  
A:Accession: C42009  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-353 <BAO>  
A:Cross-references: GB:M76673; NID:g182668; PID:g182669  
C:Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears no  
C:Genetics:  
A:Gene: GDB:FPRL2  
A:Cross-references: GDB:128855; OMIM:136539  
A:Map position: 19q13.3-19q13.4  
A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane prote  
Query Match 72.5%; Score 1318; DB 2: Length 353;  
Best Local Similarity 71.7%; Pred. No. 2.8e-103;  
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;  
QY 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIWVAGFRMTRVT 60  
DB 1 METNFTPLNEYEVSYESAGYTVLRILPLVVLGVTVFVLGVNGLVIWVAGFRMTRVT 60  
QY 61 TICYLNALADESFATLPFLIVSMAGKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TICYLNALADESFATLPFLIVSMAGKWPFGFGLCKLIHIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGWPILALVLTLPVFLFTVTTPNGDTCYTFNF 180  
DB 121 LDRICVLPVWQAQNHRTVSLAMKVIVGWPILALVLTLPVFLFTVTTPNGDTCYTFNF 180  
QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
DB 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
QY 241 RVLTVAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTVAVASFFTCWPFQVALLGVTVLWKLKEMLFYGYKIIDIIVNPTSSLAFFNSCLNPM 300  
QY 301 LVVFGQDPRERLIHSLPTSLERALS--DSAPTNDTAANSASPPAETELQAM 351  
DB 301 LVVFGQDPRERLIHSLPTSLERALS--DSAPTNDTAANSASPPAETELQAM 351  
RESULT 3  
A42009  
N-formyl peptide receptor - human  
N:Alternate names: FMLP receptor  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 14-Jul-1995 #text\_change 24-Nov-1999  
C:Accession: JC2014; A36309; A35495; A42009; I52414  
R:Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.  
Gene 133, 285-290, 1993  
A:Title: Sequence and organization of the human N-formyl peptide receptor-encoding ge  
A:Reference number: JC2014; MUID:94040825; PMID:8224916  
A:Accession: JC2014  
A:Molecule type: mRNA  
A:Residues: 1-350 <MUR>  
A:Cross-references: GB:L10820; NID:g182739; PIDN:AAAL6863.1; PID:g182740  
A:Note: 192-Asn was also found  
R:Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.  
Biochemistry 29, 11123-11133, 1990  
A:Title: The human N-formylpeptide receptor. Characterization of two cDNA isolates an  
A:Reference number: A36309; MUID:91105045; PMID:2176894  
A:Accession: A36309  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-191, 'N', 193-345, 'E', 347-350 <BOU1>  
A:Cross-references: GB:M60627; GB:M33538; NID:g182664; PIDN:AAA35847.1; PID:g182665  
R:Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.  
Biochem. Biophys. Res. Commun. 168, 1103-1109, 1990  
A:Title: Synthesis and use of a novel N-formyl peptide derivative to isolate a human  
A:Reference number: A35495; MUID:90267449; PMID:2161213  
A:Accession: A35495  
A:Molecule type: mRNA  
A:Residues: 1-100, 'L', 102-191, 'N', 193-350 <BOU2>  
A:Cross-references: GB:M37128; NID:g189183  
A:Note: the sequence in GenBank entry HUNNFP, release 112.0, (PIDN:AAA36362.1) has t  
R:Baou, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.  
Genomics 13, 437-440, 1992  
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR)  
A:Reference number: A42009; MUID:92307681; PMID:1612600  
A:Accession: A42009  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA

A:Residues: 1,'G',3-28,30-100,'L',102-104,106-112,'FLIA',115-176,178-182,184-191,'N',194  
R;Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.  
Biochemistry 31, 11955-11959, 1992  
A:Title: Cloning of the gene coding for a human receptor for formyl peptides. Characterization of the protein-coupled receptor; transmembrane protein  
A:Reference number: 152414; MUID:93075765; PMID:1445895  
A:Accession: I52414  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5 <PEP>  
A:Cross-references: GB:S49810; NID:g260832; PIDN:AA14906.1; PID:g4262758  
C:Genetics:  
A:Gene: GDB:FPRI  
A:Cross-references: GDB:127999; OMIM:136537  
A:Map position: 19q13.4-19q13.4  
A:Introns: #status absent  
A:Note: entire coding region is found in exon 3; alternatively spliced mRNA transcripts  
C:Superfamily: vertebrate rhodopsin  
F:27-53/Domain: transmembrane #status predicted <TM1>  
F:59-83/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>  
F:145-169/Domain: transmembrane #status predicted <TM4>  
F:206-225/Domain: transmembrane #status predicted <TM5>  
F:242-266/Domain: transmembrane #status predicted <TM6>  
F:279-304/Domain: transmembrane #status predicted <TM7>  
F:4,10/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:98-176/disulfide bonds: #status predicted

Query Match 68.8%; Score 1249.5; DB 2; Length 350;  
Best Local Similarity 68.9%; Pred. No. 1.6e-97;  
Matches 241; Conservative 37; Mismatches 71; Indels 1; Gaps 1;

QY 1 METNFSPLNEEYEVESAGYVLRILPLVLVGLVGVTVLGLVGLNGLVWAGFRMTRTVT 60  
Db 1 METNSSLPTNISGGTTPAVSAGYFLDITLYLFAVTVLGLVGLNGLVWAGFRMTHTVT 60

QY 61 TICVNLALADFSPTATPLPLIVSMANGKWPFCWFLCKLHIHVVDINLFGSVFLIGFIA 120  
Db 61 TISYLNALADFCFTSTLPFPFVIVTALGGHWPFGWFLCKVFTTIVDNLFGSVFLIALIA 120

QY 121 LDRICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 180  
Db 121 LDRICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 180

QY 181 ASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
Db 181 SPWTDPKERIKAVAMLTARGIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240

QY 241 RVLTVAVASFFICWFPQVALLGTWVKEMLFYGVKYYKIIDILVNPVTSLSAFAFNCLNPM 300  
Db 241 RVLTVAVASFFICWFPQVALLGTWVKEMLFYGVKYYKIIDILVNPVTSLSAFAFNCLNPM 300

QY 301 LYFVFGQDFRERLIHSLPTSLERALSDESDAPTNDTAANSAPPAETELQA 350  
Db 301 LYFVFGQDFRERLIHSLPTSLERALSDESDAPTNDTAANSAPPAETELQA 350

RESULT 4  
N-formyl peptide receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A46520  
R;Ye, R.D.; Quenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.  
J. Immunol. 150, 1383-1394, 1993  
A:Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and characterization of the protein-coupled receptor; transmembrane protein  
A:Reference number: A46520; MUID:93163563; PMID:8432984  
A:Accession: A46520  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-352 <YE1>  
A:Cross-references: GB:M94549; NID:g165027; PIDN:AAA31254.1; PID:g165028  
A:Experimental source: NZW, neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIP:124908).  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 67.3%; Score 1223.5; DB 2; Length 352;  
Best Local Similarity 67.7%; Pred. No. 2.4e-95;  
Matches 239; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

QY 1 METNFSPLNEEYEVESAGYVLRILPLVLVGLVGVTVLGLVGLNGLVWAGFRMTRTVT 60  
Db 1 MDSNASLPLNVSAGTQATPAGVLVDVFSYLLVTVTVLGLVGLNGLVWAGFRMTHTVT 60

QY 61 TICVNLALADFSPTATPLPLIVSMANGKWPFCWFLCKLHIHVVDINLFGSVFLIGFIA 120  
Db 61 TISYLNALADFSPTSTLPFPFVIVTALGGHWPFGWFLCKVFTTIVDNLFGSVFLIALIA 120

QY 121 LDRICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 178  
Db 121 LDRICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN--GDTYCTF 178

QY 179 NFASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSR 238  
Db 181 DWSPTEDPAEKLVKVAISMFMVIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSR 240

QY 239 PLRVLTVAVASFFICWFPQVALLGTWVKEMLFYGVKYYKIIDILVNPVTSLSAFAFNCLN 298  
Db 241 PLRVLTVAVASFFICWFPQVALLGTWVKEMLFYGVKYYKIIDILVNPVTSLSAFAFNCLN 299

QY 299 PMLYFVFGQDFRERLIHSLPTSLERALSDESDAPTNDTAANSAPPAETELQA 351  
Db 300 PMLYFVFGQDFRERLIHSLPTSLERALSDESDAPTNDTAANSAPPAETELQA 352

RESULT 5  
N-formyl peptide chemotactic receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A49542  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 268, 25395-25401, 1993  
A:Title: Species and subtype variants of the N-formyl peptide chemotactic receptor re-  
A:Reference number: A49542; MUID:94064602; PMID:8244972  
A:Accession: A49542  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <GAO>  
A:Cross-references: GB:L22181; NID:g347396; PIDN:AAA16110.1; PID:g347397  
C:Genetics:  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; transmembrane protein

Query Match 64.6%; Score 1174.5; DB 2; Length 364;  
Best Local Similarity 64.6%; Pred. No. 3.3e-91;  
Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

QY 1 METNFSPLNEEYEVESAGYVLRILPLVLVGLVGVTVLGLVGLNGLVWAG 52  
Db 1 MDTNLSLLMNKSAVNLNVSGTSQSVAGYIVLDVFSYLLVFAVTVLGLVGLNGLVWAG 60

QY 53 FRMTRTVTTCYLMALADFSPTATPLPLIVSMANGKWPFGWFLCKLHIHVVDINLFGS 112  
Db 61 FRMKTHTVTISYLNALADFCFTSTLPFPFVIVTALGGHWPFGWFLCKVFTTIVDNLFGS 120

QY 113 VFLIGFTALDRCICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN- 171  
Db 121 VFLIATLALDRCICVLPVWQAQNHRTVSLAMKVIIVGVPWILALVLPVFLFTTTPN- 178

QY 172 ---GDTYCTFNFASWGGTPEERLKVATMLTARGIRFVIGFSLPMSIVAICYGLIAAK 227  
Db 179 RLGPCKTACFDSPWTKDPVEKRVATMLTVRGIRFVIGFSLPMSIVAICYGLITTK 238





S65766

G protein-coupled receptor (clone A23B) - human

C:Species: Homo sapiens (man)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jul-2000

C:Accession: S65766

R:Roiglic, A.; Prossnitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.

Biochim. Biophys. Acta 1305, 39-43, 1996

A:Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular domain

A:Reference number: S65766; MUID:96180983; PMID:8605247

A:Accession: S65766

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-482 <R0G>

A:Cross-references: EMBL:U28488; NID:g1199577; PIDN:AAC50374.1; PID:g1199578

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 28.0%; Score 509.5; DB 2; Length 482;

Best Local Similarity 26.6%; Pred. No. 3.4e-35;

Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN-----FSPLNEYEVSVESAGTYVRLPLVVLGVTFVLGVGLNGLIWIWAGFMTR 57

DB 7 ETNSTDLLSPWNEPPV-----ILSMVILSUTLLGLPLNGLVWAGLKMQR 54

QY 58 TVTTCYLNIALADFSATLPLFLIVSNAMGEKPFQWFLCKLTHIVVDINLFGSVFLIG 117

DB 55 TVNTINELHLTLADLLCLLSLPSLSLAHLAQGWPGYRFLCKLIPSIIVLNMFASVELLT 114

QY 118 FIALDRICIVLHPVMAQNHRTVSLAMKVIIVGPWTLLALVLPVFLFTTTIPNGDTYCT 177

DB 115 AISUDRLVVFKEPIWCQNHRNVGMACSGICGIWVAFVMPGVFVYREIFTDHNHR-CG 173

QY 178 FNFA-----SW----- 183

DB 174 YKGLSSSLDYPDFYGDPLENRSLENTVQRPEGMNDRDPSSFOTNDHPWTVPTVPFOPQT 233

QY 184 -----GGTPEE-----R 190

DB 234 FQPSADSLPRGSARLTSQNLVSNVFKPADVVSFKPSGFPIDHETSPLDNSDAFLSTH 293

QY 191 LKV-----AITMLTARGIIRFVIGFSLPMSIVA 218

DB 294 LKLPSSASSNFYSESLPQGFQDYINLGQFTDDQVFTPLVAITITRLVVGFLPLSVIMI 353

QY 219 ICYGLIAAKTHKGWIKS-GRPLRVLTAVVAFSFFICFPFQVALLGVTLKEMFLGYKY 277

DB 354 ACYSFIVFQRGREFAKSQSKTFRVAVVAVFLVCTPYHI-----F 396

QY 278 KIIDLWNPTS-----SLAFNSCLNPMLYVFGQDFRERLIHSLPTSLER 323

DB 397 GVLSSLLDPTPLTKTLMSDHVCIALASANSFCNPFYALLGDKRKKARQSIQGLEA 456

QY 324 ALSDE-----SAPNTDAAANSAS 341

DB 457 AFSEELRSTRHCPNSNVISERN 479

RESULT 10

JC5796

probable chemoattractant receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 24-Jan-1998 #sequence\_revision 13-Mar-1998 #text\_change 20-Jun-2000

C:Accession: JC5796

R:Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.

Biochem. Biophys. Res. Commun. 241, 390-394, 1997

A:Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattractant receptor

A:Reference number: JC5796; MUID:98086361; PMID:9425281

A:Accession: JC5796

A:Molecule type: mRNA

A:Residues: 1-371 <QWM>

A:Cross-references: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398

A:Experimental source: liver

C:Comment: This protein regulates the trafficking of immune cells during a microbial chd  
C:Superfamily: vertebrate rhodopsin  
F:39-62/Domain: transmembrane #status predicted <TM1>  
F:74-94/Domain: transmembrane #status predicted <TM2>  
F:112-135/Domain: transmembrane #status predicted <TM3>  
F:156-177/Domain: transmembrane #status predicted <TM4>  
F:206-237/Domain: transmembrane #status predicted <TM5>  
F:259-280/Domain: transmembrane #status predicted <TM6>  
F:302-317/Domain: transmembrane #status predicted <TM7>  
F:7,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.7%; Score 502.5; DB 2; Length 371;  
Best Local Similarity 34.7%; Pred. No. 9.9e-35;  
Matches 120; Conservative 63; Mismatches 124; Indels 39; Gaps 9;

QY 11 EYEE-----VSESAG---YTLRLPLVVLGVTVFVLGVGLNGLVWVAGFRMTRTVTI 62  
DB 15 EYSDGDIYVDLEAGLEAKVAEFLVLYISLVCFGLGILNGLVIVATFMKKTVNTV 74  
63 CYLNLALADFSFATLPLFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALD 122  
DB 75 WEVNLAVADFELEPIHITIAADYHNVFCKAMCKISSFLSHNMVTSVFLAVISFD 134  
QY 123 RCICVLHPVWQNHRTVSLAMKVIIVGPWILALVLPFLVFLFTTIPNGDTCYCFENAS 182  
DB 135 RCISVLLPWSQNHRSVRLAYMTCVVVWVW-LSESPSPSLVFGHSTSGKITCFNFSL 193  
QY 183 WGGTPEE-----RLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI 228  
DB 194 --AAPEPFSHTPRTDPGVYGRHVAVT-----VTRFLCGFLIPVFIITACILYIVK 245  
QY 229 HKGMKISRRLVITAVVASFFICWFFPQLVALIGTFLVWLEKMLPYGKYKIIDIILNP-T 287  
DB 246 QRNRQAKTKPKKIITITITIFLCWCPYH-----TLYLLELHHTAVPASVFSGLPLA 299  
QY 288 SSIAFNSCLNPLVYVFGQDFRERLIHSLPMSIALERLSEDSAPTIN 333  
DB 300 TAVATANSCLNPLVYVFGHDFKPKV-ALFSLVNLSEDTGPSS 344

RESULT 11  
JC2492  
G protein-coupled receptor 1 - rat  
N:Alternate names: GPR-1  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999  
Accession: JC2492  
Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994  
A:Title: Mapping studies of two G protein-coupled receptor genes: An amino acid difference between the two genes  
A:Reference number: JC2492; MUID:95110347; PMID:7811287  
A:Accession: JC2492  
A:Molecule type: mRNA  
A:Residues: 1-353 <MAP>  
A:Cross-references: GB:S74702; NID:9786483; PIDN:AB32978.1; PID:g786484  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmembrane  
F:74-94/Domain: transmembrane #status predicted <TM2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:156-177/Domain: transmembrane #status predicted <TM4>  
F:206-237/Domain: transmembrane #status predicted <TM5>  
F:259-280/Domain: transmembrane #status predicted <TM6>  
F:302-317/Domain: transmembrane #status predicted <TM7>  
F:7,190/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:330/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 27.6%; Score 502; DB 2; Length 353;  
Best Local Similarity 34.2%; Pred. No. 1e-34;  
Matches 114; Conservative 72; Mismatches 123; Indels 24; Gaps 8;

QY 4 NFSTPLNEY-EVSVESAGYT-VLRILPLVVLGVTVFVLGVGLNGLVWVAGFRMTRTVTI 61  
DB 14 NYSYALEYISQEPDABENVYGVHWSISLLYALAFVLGIPGNAIVWPMFGKWKKTVT 73  
QY 62 ICYLNALADFSFATLPLFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL 121  
DB 74 LWFLNLATADFFVFLPLIYISVALSFHWPGRWLCKLNSFIAQLNMFSSVFFLIVISL 133  
QY 122 DRCICVLHPVWQNHRTVSLAMKVIIVGPWILALVLPFLVFLFTTIPNGDTCYCFENFA 181  
DB 134 DRYIHLHPGLSHPHRTLNKSLVFLVWLLASLLGGPLTYFRDIVEV-NNRIICVYNNFQ 192  
QY 182 SHGQTPERLKVATIMLTARGI--IRFVIGFSLPMSIVAICYGLIAAKIHKGMKTSR 239  
DB 193 EY-----ELTLMRHVLTWVKFLGYLLPLTLTSSCYLCLIFTKKONILISSKH 242  
QY 240 LRLVAVVASPPFCPPFQVALLGTWMLKEMLFYKGYKIIDIIL---VNPTSSLAFFNSC 296  
DB 243 LMLILSVIAFVWCVTPPHLF---SIW--ELSIHNSSFQNVLOGGIPLTGLAFLNSC 296  
QY 297 LNPMLYVFGQDFRERLIHSLPMSIALERLSEDS 329  
DB 297 LNPILYVIISKFOARFASVAELKRSIWEAS 329

RESULT 12  
S27357  
complement C5a anaphylatoxin receptor - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
Accession: S27357  
Biochem. J. 288, 911-917, 1992  
A:Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor.  
A:Reference number: S27357; MUID:93111969; PMID:1472004  
A:Accession: S27357  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352 <PER>  
A:Cross-references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879  
C:Function:  
A:Description: mediates the inflammatory and chemotactic responses of polymorphonucle  
n  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polym  
F:1-38/Domain: extracellular #status predicted <EX1>  
F:39-62/Domain: transmembrane #status predicted <TM1>  
F:63-72/Domain: intracellular #status predicted <IN1>  
F:73-95/Domain: transmembrane #status predicted <TM2>  
F:96-111/Domain: extracellular #status predicted <EX2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:134-150/Domain: intracellular #status predicted <IN2>  
F:151-175/Domain: transmembrane #status predicted <TM4>  
F:176-208/Domain: extracellular #status predicted <EX3>  
F:209-229/Domain: transmembrane #status predicted <TM5>  
F:230-244/Domain: intracellular #status predicted <IN3>  
F:245-266/Domain: transmembrane #status predicted <TM6>  
F:267-285/Domain: extracellular #status predicted <EX4>  
F:286-309/Domain: transmembrane #status predicted <TM7>  
F:310-352/Domain: intracellular #status predicted <IN4>  
F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.5%; Score 500; DB 1; Length 352;  
Best Local Similarity 31.3%; Pred. No. 1.5e-34;  
Matches 113; Conservative 75; Mismatches 133; Indels 40; Gaps 7;

QY 4 NFSTP-----LNEYEVSVESAGYVLRILPLVVLGVTVFVLGVGLNGLVWVAG 52  
DB 5 NFSPEXPDPYGTATLDPNIFVDESINTPKLSVPDMIALVIFVMVFLVGVPGNLFVWVTG 64  
QY 53 FRMTRTVTTCVNLALADFSFATLPLFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGS 112  
DB 65 FEVRTINAIWFLNLAVADLSCLALPILFSSIVQGVWFGNACRILPLSLILNMYAS 124

```
QY 113 VFLIGTALDRCICVLHPVWQAHRTVSLAMKVIQVGPWILALVLTLPVFLF--LTTVTIP 170
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 ILLTTISADRFVLVFNPNWCONYRGPOLAWACSVAVALLTVPSPFRGVHTEYFP 184
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 NGDYTCYCFNFASMGGTPEERLKVATIMLTARG--IIRFVIGFSLPMSIVAICYGLIAAKI 228
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 FWMT-CGVDSYSGV-----VLVERGVALRLMGLFGLPVLISICYFELLIRT 231
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 HKKGMIKSSRLPLRLVLTAVASFFTCWFPFQVALLGTWVKEMLFYKKYKIIDILVNPTS 288
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 WSRATRSKTKLVVAVVAVVFFVLWLPYQVTGMALFYKHSFRRVSRVLSL--CV 288
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 289 SLAFNSCLNMLYVFCQDPRERLIHSLPFLSLERALSDSA-----PTNDTANS 339
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 AVAYINCINPIIYVLAQGFHSLPARLQVLAESVGRDSKSIITLSTVDTPAQK 348
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 340 A 340
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 S 349

RESULT 13
A55733
G protein-coupled receptor GPR1 - human
C:Species: Homo sapiens (man)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
C:Accession: A55733
R:Marchese, A.; Docherty, J. M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H. H. Q.; Tsui, I.
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:95154831; PMID:7851889
A:Accession: A55733
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <MAR>
A:Cross-references: GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g577413
C:Genetics:
A:Gene: GDB:GPR1
A:Cross-references: GDB:371707; OMIM:600239
A:Map position: 15q25-15q26.1
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 27.5%; Score 499; DB 2; Length 355;
Best Local Similarity 33.3%; Pred. No. 1.9e-34;
Matches 115; Conservative 68; Mismatches 132; Indels 30; Gaps 7;

1 METNFSPLNEEVSYESAGYT-----VLRILPLVLGVTFVLGVNGGLVI 48
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MEDLEETLFEFENYSYDLDYISLESLEEKVQLGVVHWVSLVLYCLAFVIGPNAIVI 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

49 WVAGFRMTRVTTTCYLNALADFSFATLPLFLIVSMAMGEKPFPGWFLCKLIHIVVDIN 108
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 WFTGLKWKKTVTTLWFLNLALADFLFLPLLYISYVAMNFWPFGIWLCKRANSTQAQLN 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
109 LFGSVFLIGTALDRCICVLHPVWQAHRTVSLAMKVIQVGPWILALVLTLPVFLFVT 168
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 MFASVFFLTSLDHYIHLHPVLSHRHRTLKNSLIIVFIWLLASLTGGPALYFRDVE 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
169 IPNGDTYCTNFASMGGTPEERLKVATIMLTARGI--IRFVIGFSLPMSIVAICYGLIAA 226
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 F-NHHTLCYNNF-----QKHDPDITLIRHHVLTWVKFIIGYLFPLLTMSICYLCILF 231
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227 KIKHKGMIKSSRLPLRLVLTAVASFFTCWFPFQVALLGTWVKEMLFYKKYKIIDILV 284
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
232 KVKKETVLISRRHFWTILVVVAVFVWCWTPYHLP-----SIW-ELTIHNSSHVWQAGI 286
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
285 NPTSSLAFNSCLNMLYVFCQDPRERLIHSLPFLSLERALSSEDS 329
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
287 PLSTGLAFLNSCLNPILYLVLSKKFQARFRSSVAEILKYLTLEWS 331
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

## RESULT 14

```
A46525
complement C5a anaphylatoxin receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A46525
R:Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N. P.
J. Immunol. 149, 2600-2606, 1992
A:Title: Structural diversity in the extracellular faces of peptidergic G-protein-cou
A:Reference number: A46525; MUID:93017861; PMID:1401897
A:Accession: A46525
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-351 <GPR>
A:Cross-references: GB:S46665; GB:I05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
A:Experimental source: BALB/C
A:Note: sequence extracted from NCBI backbone (NCBIP:116075)
C:Function:
A:Description: mediates the inflammatory and chemotactic responses of polymorphonucle
n
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polym
F:1-37/Domain: extracellular #status predicted <EX1>
F:38-61/Domain: transmembrane #status predicted <TM1>
F:62-71/Domain: intracellular #status predicted <IN1>
F:72-94/Domain: transmembrane #status predicted <TM2>
F:95-110/Domain: extracellular #status predicted <EX2>
F:111-132/Domain: transmembrane #status predicted <TM3>
F:133-149/Domain: intracellular #status predicted <IN2>
F:150-174/Domain: transmembrane #status predicted <TM4>
F:175-207/Domain: extracellular #status predicted <EX3>
F:208-228/Domain: transmembrane #status predicted <TM5>
F:229-243/Domain: intracellular #status predicted <IN3>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:266-284/Domain: intracellular #status predicted <EX4>
F:285-308/Domain: transmembrane #status predicted <TM7>
F:309-351/Domain: intracellular #status predicted <IN4>
F:6/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.2%; Score 457.5; DB 1; Length 351;
Best Local Similarity 31.8%; Pred. No. 5.6e-31;
Matches 103; Conservative 62; Mismatches 136; Indels 23; Gaps 6;

QY 27 ILPLVLGVQTVFLVGLNGLVIVWAGFRMTRVTTTCYLNALADFSFATLPLFLIVSMA 86
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 38 VAALIIYSVFLVGVPGNALVWVTAPEFDGSPSNALFNLAVADLLSCLAMPVLTFTVL 97
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWQAHRTVSLAMKVI 146
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 NHNTWYFDATACTVLPSSLILNNKYASILLATISADRFLLVFKPIWCKVRGTGLAWMAC 157
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 VGPWILALVLTLPVFLFVTV-TIPNGDTYCTNFASMGGTPEERLKVATIMLTARGIIR 205
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 GVAVWVALLLTTPSVYREAYKDFVSEHTVCGINGG-GSPKPK-----AVAILR 207
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 206 FVIGFSLPMSIVAICYGLIAAKIHKMGMIKSSRLPLRLVLTAVVASFICWFPFQVALLGT 265
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 LMVGFVPLLTINICYTFTLLRTWSRKATSKTKLVVMAVVICFFIFLWLPYQVTGVN-I 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 266 VWLKMFLPYGVKIIDILVNPTSSLAFFNSCLNMLYVFCQDPRERLIHSLPFLSLERAL 325
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 AWLPPS---SPILKRVKELNSLCVSLAYINCCVNPYIIVYVMAAGGFHGLRLSLPSIRNAL 324
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 326 SEDSA-----PTNDTAANSA 340
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 325 SEDSVGRDSKTFPTSDTSTRKS 348
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

## RESULT 15

```
JC2134
angiotensin II receptor type 1A - rat
N:Alternate names: AT1a receptor; AT3 receptor
C:Species: Rattus norvegicus (Norway rat)
```

Db 327 HSSLSTKMSTLSYRPSDNMSSSAKPPA 353

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:15:57 ; Search time 14 Seconds  
 (without alignments)  
 1039.871 Million cell updates/sec

Title: US-09-944-807-2

Perfect score: 1817

Sequence: 1 METNFSPLNLEYEVSYESA.....TNDTANSASPPAETELQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1817	100.0	351	1	FML1_HUMAN	P25090 homo sapien
2	1782	98.1	348	1	FML1_PANTR	P79242 pan troglod
3	1781	98.0	348	1	FML1_GORGO	P79177 gorilla gor
4	1744	96.0	348	1	FML1_PONPY	P79236 pongo pygma
5	1740	95.8	348	1	FML1_MACMU	P79190 macaca mula
6	1337	73.6	351	1	FML1_MOUSE	O08790 mus musculu
7	1318	72.5	353	1	FML2_HUMAN	P25089 homo sapien
8	1312	72.2	349	1	FML2_PANTR	P79243 pan troglod
9	1304	71.8	349	1	FML2_PONPY	P79237 pongo pygma
10	1299	71.5	349	1	FML2_GORGO	P79178 gorilla gor
11	1292	71.1	349	1	FML2_MACMU	P79191 macaca mula
12	1243.5	68.4	350	1	FMLR_HUMAN	P21462 homo sapien
13	1225.5	67.4	346	1	FMLR_PANTR	P79241 pan troglod
14	1225.5	67.4	346	1	FMLR_PONPY	P79235 pongo pygma
15	1223.5	67.3	352	1	FMLR_RABIT	Q05394 oryctolagus
16	1206.5	66.4	346	1	FMLR_GORGO	P79176 gorilla gor
17	1206.5	66.4	346	1	FMLR_MACMU	P79189 macaca mula
18	1174.5	64.6	364	1	FMLR_MOUSE	P33766 mus musculu
19	553.5	30.5	356	1	GP32_HUMAN	O75388 homo sapien
20	548.5	30.2	475	1	C3AR_CAVPO	O88680 cavia porce
21	542.5	29.9	477	1	C3AR_MOUSE	O09047 mus musculu
22	538.5	29.6	371	1	CML1_MOUSE	P97468 mus musculu
23	534.5	29.4	373	1	CML1_HUMAN	Q99788 homo sapien
24	530.5	29.2	382	1	GP44_MOUSE	Q92236 mus musculu
25	530.5	29.2	473	1	C3AR_RAT	O55197 rattus norv
26	513	28.2	350	1	C5AR_HUMAN	P21730 homo sapien
27	509.5	28.0	482	1	C3AR_MOUSE	O16581 mus musculu
28	508	28.0	340	1	C5AR_GORGO	P79175 gorilla gor
29	504.5	27.8	395	1	GP44_HUMAN	Q9y544 homo sapien
30	504	27.7	340	1	C5AR_PANTR	P79240 pan troglod
31	502.5	27.7	371	1	CML1_RAT	O35786 rattus norv
32	502	27.6	353	1	GPRI_RAT	P46090 rattus norv
33	500	27.5	352	1	C5AR_CANFA	P30992 canis faml

## ALIGNMENTS

## RESULT 1

ID	FML1_HUMAN	STANDARD;	PRT;	351 AA.
AC	P25090;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	FMLP-related receptor I (FMLP-R-1) (Lipoxin A4 receptor) (LXA4			
DE	receptor) (RFP) (HM63).			
GN	FPR1 OR FPR1 OR FPR2 OR LXA4R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=92307681; PubMed=1612600;			
RA	Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;			
RT	"Mapping of genes for the human C5a receptor (C5AR), human FMLP			
RT	receptor (FPR), and two FMLP receptor homologue orphan receptors			
RT	(FPRH1, FPRH2) to chromosome 19.";			
RL	Genomics 13:437-440(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	MEDLINE=92380523; PubMed=1511907;			
RT	Perez H.D., Holmes R., Kelly E., McClary J., Andrews W.H.;			
RT	"Cloning of a cDNA encoding a receptor related to the formyl peptide			
RT	receptor of human neutrophils.";			
RL	Gene 118:303-304(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Granulocyte;			
RA	MEDLINE=92246937; PubMed=1374236;			
RA	Ye R.D., Cavanagh S.L., Quehenberger O., Prossnitz E.R.,			
RT	Cochrane C.G.;			
RT	"Isolation of a cDNA that encodes a novel granulocyte N-formyl			
RT	peptide receptor.";			
RL	Biochem. Biophys. Res. Commun. 184:582-589(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=92218423; PubMed=1373134;			
RA	Murphy P.M., Ozcelik T., Kenney R.T., Tiffany H.L., McDermott D.,			
RA	Francie U.;			
RT	"A structural homologue of the N-formyl peptide receptor.			
RT	Characterization and chromosome mapping of a peptide chemoattractant			
RT	receptor family.";			
RL	J. Biol. Chem. 267:7637-7643(1992).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Monocytes;			
RA	MEDLINE=94092629; PubMed=7505609;			
RA	Nomura H., Nielsen B.W., Matsushima K.;			
RT	"Molecular cloning of cDNAs encoding a LD78 receptor and putative			
RT	leukocyte chemotactic peptide receptors.";			
RL	Int. Immunol. 5:1239-1249(1993).			

34	499	27.5	340	1	C5AR_PONPY	P79234 pongo pygma
35	499	27.5	355	1	GPRI_HUMAN	P46091 homo sapien
36	499	27.5	355	1	GPRI_MACMU	O97664 macaca mula
37	489.5	26.9	350	1	C5AR_RABIT	Q9tuel oryctolagus
38	486	26.7	352	1	C5AR_RAT	P97520 rattus norv
39	483.5	26.6	340	1	C5AR_MACMU	P79188 macaca mula
40	472	26.0	339	1	GP33_MOUSE	O88416 mus musculu
41	458	25.2	347	1	C5AR_MOUSE	P30993 mus musculu
42	441	24.3	345	1	C5AR_CAVPO	O70129 cavia porce
43	434	23.9	356	1	IL8B_CANFA	O97571 canis faml
44	433	23.8	353	1	CCR4_FELCA	P56498 felis silve
45	430.5	23.7	359	1	AG2R_CAVPO	Q9wv26 cavia porce

RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Maddox J.F., Hachicha M., Takano T., Petasis N.A., Fokin V.V.,  
 RL Serban C.N.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98215774; PubMed=9547339;  
 RA Gronert K., Gewirtz A., Madara J.L., Serhan C.N.;  
 RT "Identification of a human enterocyte lipoxin A4 receptor that is  
 regulated by interleukin (IL)-13 and interferon gamma and inhibits  
 tumor necrosis factor alpha-induced IL-8 release";  
 RL J. Exp. Med. 187:1285-1294 (1998).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,  
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=97296322; PubMed=9151906;  
 RA Takano T., Fiore S., Maddox J.F., Brady H.R., Petasis N.A.,  
 RA Serban C.N.;  
 RT "Aspirin-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues  
 are potent inhibitors of acute inflammation: evidence for  
 anti-inflammatory receptors";  
 RL J. Exp. Med. 185:1693-1704 (1997).  
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,  
 WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THE  
 ACTIVATION OF LXA4R COULD RESULT IN AN ANTI-INFLAMMATORY OUTCOME  
 COUNTERACTING THE ACTIONS OF PROINFLAMMATORY SIGNALS SUCH AS LTB4  
 (LEUKOTRIENE B4).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN THE LUNG AND  
 NEUTROPHILS. ALSO FOUND IN THE SPLEEN AND TESTIS.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M76672; AAA58481.1; -;  
 DR EMBL; X63819; CAA45319.1; -;  
 DR EMBL; M88107; AAA60070.1; -;  
 DR EMBL; M84562; AAA52473.1; -;  
 DR EMBL; U10922; BAA01720.1; -;  
 DR EMBL; U81501; AAB51133.1; -;  
 DR EMBL; AF054013; AAC13684.1; -;  
 DR EMBL; AC018755; AAF87844.1; -;  
 DR PIR; JC1258; JC1258.  
 DR PIR; A42492; A42492.  
 DR PIR; JQ1521; JQ1521.  
 DR PIR; B42009; B42009.  
 DR HSSP; P34996; 1DDD.  
 DR Genew; HGNC:3827; FPRLL1.  
 DR MIM; 136538; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.

DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 Chemotaxis.  
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 28 50 1 (POTENTIAL).  
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 62 83 2 (POTENTIAL).  
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 121 3 (POTENTIAL).  
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 141 162 4 (POTENTIAL).  
 FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 206 226 5 (POTENTIAL).  
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 243 266 6 (POTENTIAL).  
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 287 306 7 (POTENTIAL).  
 FT DOMAIN 307 351 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 98 176 POTENTIAL.  
 FT CONFLICT 339 S -> C (IN REF. 1).  
 SQ SEQUENCE 351 AA; 38964 MW; DC6A1D77AFC0D780 CRC64;  
 Query Match 100.0%; Score 1817; DB 1; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 1e-97;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METNESTPLNEEYEEVSAGYTVLRILPLVVLGVTVFVLGVLGNGLVIVVAGFRMTRTVT 60  
 DB 1 METNESTPLNEEYEEVSAGYTVLRILPLVVLGVTVFVLGVLGNGLVIVVAGFRMTRTVT 60  
 QY 61 TICYLNALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
 DB 61 TICYLNALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
 QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGFWILALVLTLPVFLFVLTVPNGDTCYTFNF 180  
 DB 121 LDRICVLPVWQAQNHRTVSLAMKVIVGFWILALVLTLPVFLFVLTVPNGDTCYTFNF 180  
 QY 181 ASWGCTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPL 240  
 DB 181 ASWGCTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPL 240  
 QY 241 RVLTVAVASFFTCWPPFQVALLGTWVKEMLFYGYKIIDIILVNPTSSLAFFNSCLNPM 300  
 DB 241 RVLTVAVASFFTCWPPFQVALLGTWVKEMLFYGYKIIDIILVNPTSSLAFFNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSSEDSAPTNDTAANSASPPAETELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSSEDSAPTNDTAANSASPPAETELQAM 351

## RESULT 2

FML1\_PANTR  
 ID FML1\_PANTR STANDARD; PRT; 348 AA.  
 AC P79242;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).  
 GN FPRLL.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96421539; PubMed=8824156;  
 RA Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.;  
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in  
 non-human primates";  
 RL Immunogenetics 44:446-452 (1996).  
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,

CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X97739; CAA66323.1; -;  
 CC HSP; P34996; IDDD.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_FL1; 1.  
 CC PROSITE; PS0262; G\_PROTEIN\_RECEPTOR\_FL2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Chemotaxis.  
 CC  
 CC NON\_TER 1 1  
 CC DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 25 47 1 (POTENTIAL).  
 CC DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 59 80 2 (POTENTIAL).  
 CC DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 98 118 3 (POTENTIAL).  
 CC DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 138 159 4 (POTENTIAL).  
 CC DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 203 223 5 (POTENTIAL).  
 CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 240 263 6 (POTENTIAL).  
 CC DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 284 303 7 (POTENTIAL).  
 CC DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 CC CARBOHYD 1 1 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC DISULFID 95 173  
 CC NON\_TER 348 348  
 CC SEQUENCE 348 AA; 38574 MW; 55B76670DF4D594E CRC64;

Query Match 98.1%; Score 1782; DB 1; Length 348;  
 Best Local Similarity 98.9%; Pred. No. le-95;  
 Matches 344; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 4 NFSTPLNEYEVESAGYTVLRILPLVLGVTVFVLGVGLVWAGFRMTRIVTTTC 63  
 1 NFSTPLNEYEVESAGYTVLRILPLVLGVTVFVLGVGLVWAGFRMTRIVTTTC 60  
 64 YNLALADFSFATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 123  
 61 YNLALADFSFATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 120  
 124 CICVLHPWAQNHRTVSLAMKVIIVGPWILALVLPFLFTTTPINGDYCTCFNFASW 183  
 121 CICVLHPWAQNHRTVSLAMKVIIVGPWILALVLPFLFTTTPINGDYCTCFNFASW 180  
 184 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIIVACVGLIAAKTHKGMKSSRPLRLV 243  
 181 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIIVACVGLIAAKTHKGMKSSRPLRLV 240  
 244 TAVVASFFICWFPFQVALLGTVMKEMLFYKGYKIIIDILVNPSTSSLAFFNSCLNPMILV 303  
 241 TAVVASFFICWFPFQVALLGTVMKEMLFYKGYKIIIDILVNPSTSSLAFFNSCLNPMILV 300  
 304 FVGQDFRRLHLSLPTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
 301 FVGQDFRRLHLSLPTSLERALSSEDAPTNDTAANSAPPAETELQAM 348

RESULT 3  
 FMLL\_GORGO STANDARD; PRT; 348 AA.  
 AC P79177;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).  
 GN FPLLI.  
 OS Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96421539; PubMed=8824156;  
 RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;  
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in  
 RT non-human primates.";  
 RL Immunogenetics 44:446-452(1996).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,  
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 CC EMBL; X97738; CAA66322.1; -;  
 CC HSP; P34996; IDDD.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_FL1; 1.  
 CC PROSITE; PS0262; G\_PROTEIN\_RECEPTOR\_FL2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Chemotaxis.  
 CC NON\_TER 1 1  
 CC DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 25 47 1 (POTENTIAL).  
 CC DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 59 80 2 (POTENTIAL).  
 CC DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 98 118 3 (POTENTIAL).  
 CC DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 138 159 4 (POTENTIAL).  
 CC DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 203 223 5 (POTENTIAL).  
 CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 240 263 6 (POTENTIAL).  
 CC DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 284 303 7 (POTENTIAL).  
 CC DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 CC CARBOHYD 1 1 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC DISULFID 95 173  
 CC NON\_TER 348 348  
 CC SEQUENCE 348 AA; 38580 MW; B1F0B3BDCC76CAA0 CRC64;  
 Query Match 98.0%; Score 1781; DB 1; Length 348;  
 Best Local Similarity 98.9%; Pred. No. 1.2e-95;  
 Matches 344; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 4 NFSTPLNEYEVESAGYTVLRILPLVLGVTVFVLGVGLVWAGFRMTRIVTTTC 63  
 1 NFSTPLNEYEVESAGYTVLRILPLVLGVTVFVLGVGLVWAGFRMTRIVTTTC 60

QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 |||||  
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120  
 |||||  
 QY 124 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 183  
 |||||  
 DB 121 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 180  
 |||||  
 QY 184 GGTPEERLKVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243  
 |||||  
 DB 181 GGTPEERKQVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240  
 |||||  
 QY 244 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 303  
 |||||  
 DB 241 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 300  
 |||||  
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
 |||||  
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348  
 |||||

## RESULT 4

FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 203 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 263 6 (POTENTIAL).  
 FT DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 284 303 7 (POTENTIAL).  
 FT DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 95 173 POTENTIAL.  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38686 MW; ES44D005CFA41616 CRC64;  
 Query Match 96.0%; Score 1744; DB 1; Length 348;  
 Best Local Similarity 96.6%; Pred. No. 1.5e-93;  
 Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 63  
 |||||  
 DB 1 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 60  
 |||||  
 QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 |||||  
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120  
 |||||  
 QY 124 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 183  
 |||||  
 DB 121 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 180  
 |||||  
 QY 184 GGTPEERLKVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243  
 |||||  
 DB 181 GGTPEERKQVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240  
 |||||  
 QY 244 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 303  
 |||||  
 DB 241 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 300  
 |||||  
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
 |||||  
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348  
 |||||

RESULT 5  
 FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 203 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 263 6 (POTENTIAL).  
 FT DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 284 303 7 (POTENTIAL).  
 FT DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 95 173 POTENTIAL.  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38686 MW; ES44D005CFA41616 CRC64;  
 Query Match 96.0%; Score 1744; DB 1; Length 348;  
 Best Local Similarity 96.6%; Pred. No. 1.5e-93;  
 Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 63  
 |||||  
 DB 1 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 60  
 |||||  
 QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 |||||  
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120  
 |||||  
 QY 124 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 183  
 |||||  
 DB 121 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 180  
 |||||  
 QY 184 GGTPEERLKVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243  
 |||||  
 DB 181 GGTPEERKQVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240  
 |||||  
 QY 244 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 303  
 |||||  
 DB 241 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 300  
 |||||  
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
 |||||  
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348  
 |||||

RESULT 5  
 FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 203 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 263 6 (POTENTIAL).  
 FT DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 284 303 7 (POTENTIAL).  
 FT DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 95 173 POTENTIAL.  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38686 MW; ES44D005CFA41616 CRC64;  
 Query Match 96.0%; Score 1744; DB 1; Length 348;  
 Best Local Similarity 96.6%; Pred. No. 1.5e-93;  
 Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 63  
 |||||  
 DB 1 NFSTPLNEVEEVSAGTYVLRILPLVVLGYTFVLGVGLNGLVIVWAGFRMTRVTTC 60  
 |||||  
 QY 64 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 |||||  
 DB 61 YLNALADSFSTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120  
 |||||  
 QY 124 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 183  
 |||||  
 DB 121 CICVLHPVNAQHRTVSLAMKVIIVGFWILALVLTLPVFLFTVTPNGDTCYCFENFASW 180  
 |||||  
 QY 184 GGTPEERLKVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 243  
 |||||  
 DB 181 GGTPEERKQVAITMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL 240  
 |||||  
 QY 244 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 303  
 |||||  
 DB 241 TAVASFFICWPFQVALLGVWVKEMLFYGYKYIIDILVNPTSSLAFFNSCLNPMYLV 300  
 |||||  
 QY 304 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
 |||||  
 DB 301 FVGQDFRERLIHSLTSLERALSSEDAPTNDTAANSAPPAETELQAM 348  
 |||||

RESULT 5  
 FT DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 203 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 263 6 (POTENTIAL).  
 FT DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 284 303 7 (POTENTIAL).  
 FT DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 1 1 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 95 173 POTENTIAL.  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38686 MW; ES44D005CFA41616 CRC64;  
 Query Match 96.0%; Score 1744; DB 1; Length 348;  
 Best Local Similarity 96.6%; Pred. No. 1.5e-93;  
 Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;



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EMBL: X97737; CAA66321.1; -.  
HSP: P34996; IDD.  
InterPro: IPR000276; GPCR\_Rhodpsn.  
Pfam: PF00001; 7tm\_1; 1.  
PROSITE: PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
PROSITE: PS00262; G\_PROTEIN\_RECEPTOR\_F2\_1; 1.  
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.  
NON\_TER 1 1  
DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).  
DOMAIN 45 47 1 (POTENTIAL).  
DOMAIN 28 58 CYTOPLASMIC (POTENTIAL).  
DOMAIN 59 80 2 (POTENTIAL).  
DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).  
DOMAIN 98 118 3 (POTENTIAL).  
DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).  
DOMAIN 138 159 4 (POTENTIAL).  
DOMAIN 160 202 EXTRACELLULAR (POTENTIAL).  
DOMAIN 203 223 5 (POTENTIAL).  
DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
DOMAIN 240 263 6 (POTENTIAL).  
DOMAIN 264 283 EXTRACELLULAR (POTENTIAL).  
DOMAIN 284 303 7 (POTENTIAL).  
DOMAIN 304 348 CYTOPLASMIC (POTENTIAL).  
CARBOHYD 1 1 N-LINKED (GLCNAC. . .) (POTENTIAL).  
DISULFID 95 173  
NON\_TER 348 348  
SEQUENCE 348 AA; 38456 MW; BC185DFAC14B694E CRC64;

Query Match 95.8%; Score 1740; DB 1; Length 348;  
Best Local Similarity 96.68; Pred. No. 2.6e-93;  
Matches 336; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NFSPLNEEYVESAGYVLRILPLVGLVGVTFVGLVGLNGLVWAGFRMTRVTVIC 63  
Db 1 NFSPLNEEYVESAGYVLRILPLVGLVGVTFVGLVGLNGLVWAGFRMTRVTVIC 60  
Qy 64 YLNALADFSFATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 123  
Db 61 YLNALADFSFATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDR 120  
Qy 124 CICVLHPVWAGNHRVSLAMKVIIVGPPWILALVLPVFLFTTVPNGDYCYTFNFASW 183  
Db 121 CICVLHPVWAGNHRVSLAMKVIIVGPPWILALVLPVFLFTTVPNGDYCYTFNFASW 180  
Qy 184 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPLRVL 243  
Db 181 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPLRVL 240  
Qy 244 TAVVASFICFPQVALLGTWVKMLFYGKYKIIDILVNPVSSLAFFNSCLNPMLYV 303  
Db 241 TAVVASFICFPQVALLGTWVKMLFYGKYKIIDILVNPVSSLAFFNSCLNPMLYV 300  
Qy 304 FVGQDFRERLHSLPTSLERALSSEDAPTNDTAANSAPPAETELQAM 351  
Db 301 FVGQDFRERLHSLPTSLERALSSEDAPTNDTAANSAPPAETELQAM 348  
RESULT 6  
FML1\_MOUSE  
ID FML1\_MOUSE STANDARD; PRT; 351 AA.  
AC 008790;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE FMLP-related receptor I (FMLP-R-I) (Lipoxin A4 receptor) (LXA4 receptor).  
GN FPLI OR LXA4R.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RC SEQUENCE FROM N.A.  
RC TISSUE=Spleen, and Neutrophils;  
RX MEDLINE=97296322; PubMed=9151906;  
RA Takano T., Fiore S., Maddox J.F., Brady H.R., Petasis N.A.,  
RA Serhan C.N.;  
RT "Aspirin-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues  
RT are potent inhibitors of acute inflammation: evidence for anti-  
RT inflammatory receptors";  
RL J. Exp. Med. 185:1693-1704(1997).  
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,  
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THE  
CC ACTIVATION OF LXA4R COULD RESULT IN AN ANTI-INFLAMMATORY OUTCOME  
CC COUNTERACTING THE ACTIONS OF PROINFLAMMATORY SIGNALS SUCH AS LTB4  
CC (LEUKOTRIENE B4).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED MOSTLY IN NEUTROPHILS, FOLLOWED BY  
CC SPLEEN AND LUNG. EXPRESSED AT VERY LOW LEVELS IN HEART AND LIVER.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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EMBL: U78299; AAC53198.1; -.  
MGD: MGI:1194495; Pp11.  
InterPro: IPR000276; GPCR\_Rhodpsn.  
Pfam: PF00001; 7tm\_1; 1.  
PRINTS: PR00237; GPCR\_HODOPSIN.  
PROSITE: PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
PROSITE: PS00262; G\_PROTEIN\_RECEPTOR\_F2\_1; 1.  
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.  
DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
TRANSMEM 28 50 1 (POTENTIAL).  
DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).  
TRANSMEM 62 83 2 (POTENTIAL).  
DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).  
TRANSMEM 101 121 3 (POTENTIAL).  
DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).  
TRANSMEM 141 162 4 (POTENTIAL).  
DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).  
TRANSMEM 206 226 5 (POTENTIAL).  
DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).  
TRANSMEM 243 266 6 (POTENTIAL).  
DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).  
TRANSMEM 287 306 7 (POTENTIAL).  
DOMAIN 307 351 CYTOPLASMIC (POTENTIAL).  
CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).  
DISULFID 98 176  
SEQUENCE 351 AA; 39548 MW; 1AF3B374B195E0CB CRC64;

Query Match 73.6%; Score 1337; DB 1; Length 351;  
Best Local Similarity 73.28; Pred. No. 3e-70;  
Matches 257; Conservative 29; Mismatches 65; Indels 0; Gaps 0;

Qy 1 METNFTPLNEEYVESAGYVLRILPLVGLVGVTFVGLVGLNGLVWAGFRMTRVTVIC 60  
Db 1 MESNYSIHNGSEVVYDTSIRVLWSVVVSITFFGLVGLNGLVWAGFRMTRVTVIC 60  
Qy 61 TICYNLALADFSFATLPFLIVSMANGKWPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120

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Db 61 TWYLNALADESFATLFLVLIVEMAKKWPFGFLCKLVHADVNFVSGVFLIAVIA 120
QY 121 LDRICVLPVWQAQNRHTVSLAMKVIWGPWILALVLTLPVFLFLLTTPVTPNGDTCYTFNF 180
Db 121 LDRICVLPVWQAQNRHTVSLAMKVIWGPWILALVLTLPVFLFLLTTPVTPNGDTCYTFNF 180
QY 181 ASWGGTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGKMSRRL 240
Db 181 VSGNSVEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGKMSRRL 240
QY 241 RVLTAVASFFTCWPFQVALLGVWVKEMLFYKGYKIIDLIVNPTSSLAFFNSCLNPM 300
Db 241 RVLTAVASFFTCWPFQVALLGVWVKEMLFYKGYKIIDLIVNPTSSLAFFNSCLNPM 300
QY 301 LYVFGQDFRERLIHSLPTSLERLSEDSAPTNDTAANSAPPAETELQAM 351
Db 301 LYVFGQDFRERLIHSLPTSLERLSEDSAPTNDTAANSAPPAETELQAM 351

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## RESULT 7

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ID FML2_HUMAN STANDARD; PRT; 353 AA.
AC P25089;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE FMLP-related receptor II (FMLP-R-II).
GN FPR1L2 OR FPRH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307681; PubMed=1612600;
RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;
RT "Mapping of genes for the human C5a receptor (C5AR), human FMLP
RT receptor (FPR), and two FMLP receptor homologue orphan receptors
RT (FPRH1, FPRH2) to chromosome 19."
RL Genomics 13:437-440(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256976; PubMed=8198572;
RA Durstun M., Gao J.-L., Tiffany H.L., McDermott D., Murphy P.M.;
RT "Differential expression of members of the N-formylpeptide receptor
RT gene cluster in human phagocytes."
RL Biochem. Biophys. Res. Commun. 201:174-179(1994).
CC -!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC -----
CC EMBL; M76573; AAA58482.1; -.
CC EMBL; L14061; AAA52474.1; -.
CC PIR; C42009; C42009.
CC Genbank; HGNC:3828; FPR1L2.
CC MIM; 136539; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 61 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT CONFLICT 94 94 A -> G (IN REF. 2).
FT CONFLICT 211 211 T -> S (IN REF. 2).
FT CONFLICT 338 338 H -> D (IN REF. 2).
SQ SEQUENCE 353 AA; 40015 MW; 8ED7450A14A36C9A CRC64;

Query Match 72.5%; Score 1318; DB 1; Length 353;
Best Local Similarity 71.7%; Pred. No. 3.7e-69;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNSTPLNEEVEYSYSGATVRLPLVVLVGVTVTVLGVGLNGLVIVWAGFRMTRVT 60
DB 1 METNFSIPLNETEEVLPBPAGHTVLWIFSLVHGVTFVGVGLNGLVIVWAGFRMTRVN 60
QY 61 TICYNLALADESFATLFLVLIVEMAKKWPFGFLCKLVHADVNFVSGVFLIGFTA 120
DB 61 TICYNLALADESFATLFLVLIVEMAKKWPFGFLCKLVHADVNFVSGVFLITIIA 120
QY 121 LDRICVLPVWQAQNRHTVSLAMKVIWGPWILALVLTLPVFLFLLTTPVTPNGDTCYTFNF 180
DB 121 LDRICVLPVWQAQNRHTVSLAMKVIWGPWILALVLTLPVFLFLLTTPVTPNGDTCYTFNF 180
QY 181 ASWGGTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGKMSRRL 240
DB 181 ASWGGTPEERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMGKMSRRL 240
QY 241 RVLTAVASFFTCWPFQVALLGVWVKEMLFYKGYKIIDLIVNPTSSLAFFNSCLNPM 300
DB 241 RVLTAVASFFTCWPFQVALLGVWVKEMLFYKGYKIIDLIVNPTSSLAFFNSCLNPM 300
QY 301 LYVFGQDFRERLIHSLPTSLERLSEDSAPTNDTAANSAPPAETELQAM 351
DB 301 LYVFGQDFRERLIHSLPTSLERLSEDSAPTNDTAANSAPPAETELQAM 351

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## RESULT 8

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ID FML2_PANTR STANDARD; PRT; 349 AA.
AC P79243;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-formyl peptide receptor-like 2 receptor (Fragment).
GN FPR1L2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehén F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in

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non-human primates *;
Immunogenetics 44:446-452(1996).
-1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
FMPL TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL: X97743; CAA66327.1; -.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PROSITE: PS00237; G-PROTEIN_RECF1_1; 1.
PROSITE: PS0262; G-PROTEIN_RECF1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemotaxis.
DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
TRANSMEM 28 50 1 (POTENTIAL).
DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
TRANSMEM 62 83 2 (POTENTIAL).
DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
TRANSMEM 101 121 3 (POTENTIAL).
DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
TRANSMEM 141 162 4 (POTENTIAL).
DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
TRANSMEM 206 226 5 (POTENTIAL).
DOMAIN 227 242 6 (POTENTIAL).
TRANSMEM 243 266 7 (POTENTIAL).
DOMAIN 267 286 CYTOPLASMIC (POTENTIAL).
TRANSMEM 287 306 7 (POTENTIAL).
DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
DISULFID 98 176 POTENTIAL.
NON_TER 349 349
SEQUENCE 349 AA; 88279F8C72915383 CRC64;

Query Match 72.2%; Score 1312; DB 1; Length 349;
Best Local Similarity 72.2%; Pred. No. 8e-69;
Matches 252; Conservative 37; Mismatches 58; Indels 2; Gaps 1;

Qy 1 METNFTPLNEYEVESYAGYTVLRILPLVLGVVTVFVGLVGLNGLVWVAGFRMTRVT 60
Db 1 METNFSIPLNSEEVLPFAGHTVLIWIFSLVHGVTVFVGLVGLNGLVWVAGFRMTRVN 60
Qy 61 TICVNLALADFSFATLPELIVSMGCEKWPFCNFKLHIVVDINLFGSVFLIGFIA 120
Db 61 TICVNLALADFSFATLPELIVSMGCEKWPFCNFKLHIVVDINLFGSVFLIGFIA 120
Qy 121 LDRICCVLHPWAQNHRTVSAMKVIYGVFWILALVLTLPVFLFTTVTPNGDYCYTFNF 180
Db 121 LDRICCVLHPWAQNHRTVSAMKVIYGVFWILALVLTLPVFLFTTVTPNGDYCYTFNF 180
Qy 181 ASWGGTPPEERKVAITMTARGITRFVGFSLPMSIVAICYGLIAAKTHKKGMKSSRPL 240
Db 181 ASWGGTPPEERKVAITMTARGITRFVGFSLPMSIVAICYGLIAAKTHKKGMKSSRPL 240
Qy 181 AFWGDTAVERNVFTAKVFLILHFIIGFSPMPSIIIVCYGIIAAKTHRNMIKSSRPL 240
Db 181 AFWGDTAVERNVFTAKVFLILHFIIGFSPMPSIIIVCYGIIAAKTHRNMIKSSRPL 240
Qy 241 RVLTAVASFTICFPFOLVALLGVNLMKFLFYCKYKIIIDLVNPTSSLAFFNSCLNPM 300
Db 241 RVLTAVASFTICFPFOLVALLGVNLMKFLFYCKYKIIIDLVNPTSSLAFFNSCLNPM 300
Qy 301 LYFVGGDFRRLHSLPTSLERALSE--DSAPTNDTAAANSPPAETE 347
Db 301 LYFVGGDFRRLHSLPTSLERALSE--DSAPTNDTAAANSPPAETE 347
Qy 301 LYFVGRNFRRLHSLPTSLERALSE--DSAPTNDTAAANSPPAETE 349
Db 301 LYFVGRNFRRLHSLPTSLERALSE--DSAPTNDTAAANSPPAETE 349

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RESULT 9
FML2_PONPY STANDARD; PRT; 349 AA.
AC P79237;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-formyl peptide receptor-like 2 receptor (Fragment).
GN FPRL2.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID:9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96421539; PubMed:88241156;
RT Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RL "Molecular evolution of the N-formyl peptide and C5a receptors in
non-human primates.";
IMMUNOGENETICS 44:446-452(1996).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
FMPL TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL: X97741; CAA66325.1; -.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PROSITE: PS00237; G-PROTEIN_RECF1_1; 1.
PROSITE: PS0262; G-PROTEIN_RECF1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemotaxis.
DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
TRANSMEM 28 50 1 (POTENTIAL).
DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
TRANSMEM 62 83 2 (POTENTIAL).
DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
TRANSMEM 101 121 3 (POTENTIAL).
DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
TRANSMEM 141 162 4 (POTENTIAL).
DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
TRANSMEM 206 226 5 (POTENTIAL).
DOMAIN 227 242 6 (POTENTIAL).
TRANSMEM 243 266 6 (POTENTIAL).
DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
TRANSMEM 287 306 7 (POTENTIAL).
DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
DISULFID 98 176 POTENTIAL.
NON_TER 349 349
SEQUENCE 349 AA; 39423 MW; C8298D223395EECB CRC64;

Query Match 71.8%; Score 1304; DB 1; Length 349;
Best Local Similarity 71.8%; Pred. No. 2.3e-68;
Matches 250; Conservative 39; Mismatches 58; Indels 2; Gaps 1;

Qy 1 METNFTPLNEYEVESYAGYTVLRILPLVLGVVTVFVGLVGLNGLVWVAGFRMTRVT 60
Db 1 METNFSIPLNSEEVLPFAGHTVLIWIFSLVHGVTVFVGLVGLNGLVWVAGFRMTRVN 60

```

FT	DOMAIN	163	205	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	206	226	5 (POTENTIAL).	
FT	DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).	
FT	TRANSSEM	243	266	6 (POTENTIAL).	
FT	DOMAIN	267	286	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	287	306	7 (POTENTIAL).	
FT	DOMAIN	307	>349	CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	DISULFID	98	176	POTENTIAL.	
FT	NON_TER	349	349		
SQ	SEQUENCE	349 AA;	39432 MW;	C6ED77CFDE023834 CRC64;	

  

Query Match	71.5%;	Score 1299;	DB 1;	Length 349;
Best Local Similarity	71.3%;	Pred. No. 4.4e-68;		
Matches 249;	Conservative 38;	Mismatches 60;	Indels 2;	Gaps

  

QY	1	MEINFSTPLNMEYBEVYESAGYTVLRILPLVLVLGVGVFLVGLVGNGLVWVAGFRMTRTVT	60
DB	1	MEINFSTPLNTEEVLPEPAGHTVLFISLLVHGVTFFICVLGNGLVWVAGFLMTRTVN	60
QY	61	TICYLNLALADFSTAYPLPLIVSMAMGEKWPGEFLCKLIHIVVDINLFGSVFLIGFTA	120
DB	61	TICYLNLALADFSAIPLPHMYSVAMREKWPGEFLCKLVHVMIDINLFGSVYLITIA	120
QY	121	LDRICICVLHPVAQNHTVSLAMKVIIVGPMILALVLTFLVPFLTFTVTLPNGDGYCTENF	180
DB	121	LDRICICVLHPVAQNHTVSLAKRVMTGLWILTVLTFNPFWTITSTNGDTYICFNF	180
QY	181	ASNGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMIKSSRPL	240
DB	181	PWGDTRAVERNLVFITMAKVFLLHFIIGFSMPMSIITVCYGTIAAKIHKNHMIKSSRPL	240
QY	241	RVLTAVVAVSFICWFPFQVALLGTVLWEMLFYGYKKIIDILVNPTSSLAFFNSCLNPM	300
DB	241	RVFAAVVAVSFICWFPFYELIGILIMVWLKEMLNGYKYLIVLINTPSSLAFFNSCLNPI	300
QY	301	LYYFVGQDFRERLIHSPTSLERALSE--DSAPTNDTAANSAPPAETE	347
DB	301	LYYVFLGNSQERLIIRSLPTSLERALTEVPDSQTSNHTHTSAPPEETE	349

  

RESULT 11	FML2_MACMU	STANDARD;	PRT;	349 AA.
ID	FML2_MACMU			
AC	P79191;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DE	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	N-formyl peptide receptor-like 2 receptor (Fragment).			
GN	FPRL2.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
ON	NCBI_Taxid=9544;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=96421539; PubMed=8824156;			
RA	Alvarez V., Coto E., Selen F., Gouzalet-Koces S., Lopez-Larrea C.;			
RT	"Molecular evolution of the N-formyl peptide and c5a receptors in non-human primates."			
RL	Immunogenetics 44:446-452(1996).			
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collabor			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstat			

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EMBL: X97740; CAA66324.1; -  
InterPro: IPR000276; GPCR\_Rhodpsn.  
Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_FL2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
Chemotaxis.  
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 28 50 1 (POTENTIAL).  
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 62 83 2 (POTENTIAL).  
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 101 121 3 (POTENTIAL).  
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 141 162 4 (POTENTIAL).  
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 206 226 5 (POTENTIAL).  
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 243 266 6 (POTENTIAL).  
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 287 306 7 (POTENTIAL).  
FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT DISULFID 98 176 POTENTIAL.  
FT NON\_TER 349 349  
SQ SEQUENCE 349 AA; 39531 MW; C0C92A9B5CDE250C CRC64;

Query Match 71.1%; Score 1292; DB 1; Length 349;  
Best Local Similarity 70.5%; Pred. No. 1.1e-67;  
Matches 246; Conservative 39; Mismatches 62; Indels 2; Gaps 1;

QY 1 METNFTPLNEYEVSYESAGYVLRILPLVLGVTVFVLGVLGVLVWAGFRMTRVT 60  
Db 1 METNFTPLNEYEVSYESAGYVLRILPLVLGVTVFVLGVLGVLVWAGFRMTRVT 60  
QY 61 TICVNLALADFSATLPLFLIVSMANGKWPFGWFKLHLHYVDNLNFGSVPLIGFIA 120  
Db 61 TICVNLALADFSATLPLFLIVSMANGKWPFGWFKLHLHYVDNLNFGSVPLIGFIA 120  
QY 121 LDRICVLPVWQAQNHRTVSLAMKVIVGVPTIALVLPLVPLFTVTTPNGDYCTCFNF 180  
Db 121 LDRICVLPVWQAQNHRTVSLAMKVIVGVPTIALVLPLVPLFTVTTPNGDYCTCFNF 180  
QY 181 ASWGGTPEERLKVATMLTARGITRFVIGSLPMSVAICVGLIAAKIHKMGTKSSRPL 240  
Db 181 ASWGGTPEERLKVATMLTARGITRFVIGSLPMSVAICVGLIAAKIHKMGTKSSRPL 240  
QY 241 RVLTAVASFFICWPFQVALLGTVLWVGLVGVGVGVGVGVGVGVGVGVGVGVGVGV 300  
Db 241 RVLTAVASFFICWPFQVALLGTVLWVGLVGVGVGVGVGVGVGVGVGVGVGVGVGV 300  
QY 301 LYFVVGQDFRRLRHLISLPTSLERALSE-DSAPTNDTAANSASPAETE 347  
Db 301 LYFVVGQDFRRLRHLISLPTSLERALSE-DSAPTNDTAANSASPAETE 347

RESULT 12

FMLR\_HUMAN  
ID FMLR\_HUMAN STANDARD; PRT; 350 AA.  
AC P21462; O14939; Q9NS48;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, last sequence update)  
DT 15-JUN-2002 (Rel. 41, last annotation update)  
DE fmet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)  
DE (fPR) (N-formyl peptide chemoattractant receptor).  
GN FPR1.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-90267449; PubMed-2161213;  
RA Boulay F., Tardif M., Bouchon L., Vignais P.;  
RT "Synthesis and use of a novel N-formyl peptide derivative to isolate  
RT a human N-formyl peptide receptor cDNA.";  
RL Biochem. Biophys. Res. Commun. 168:1103-1109(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91105045; PubMed-2176894;  
RA Boulay F., Tardif M., Bouchon L., Vignais P.;  
RT "The human N-formylpeptide receptor. Characterization of two cDNA  
RT isolates and evidence for a new subfamily of G-protein-coupled  
RT receptors.";  
RL Biochemistry 29:11123-11133(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91286286; PubMed-1712023;  
RA Murphy P.M., McDermott D.;  
RT "Functional expression of the human formyl peptide receptor in  
RT Xenopus oocytes requires a complementary human factor.";  
RL J. Biol. Chem. 266:12560-12567(1991).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Perez H.D.;  
RT Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-94040825; PubMed-8224916;  
RA Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;  
RT "Sequence and organization of the human N-formyl peptide receptor-  
RT encoding gene.";  
RL Gene 133:285-290(1993).  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McGready P.M., Skowronski E., Viswanathan V.,  
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,  
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Andreise T., Frankheim M., Atlix C., Amico-Keller G., Coeffield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of a 5-Mb region in 19q13.4.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Straussberg R.;  
RT TISSUE-Kidney;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,  
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: NEUTROPHILS.  
CC -1- POLYMORPHISM: THE VARIANT SEQUENCES ARE THOUGHT TO BE DUE TO  
CC ALLELIC VARIATION OF A SINGLE GENE.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR	EMBL; M37128; AAA36362.1; -	
DR	EMBL; M60626; AAA35846.1; -	
DR	EMBL; M60627; AAA35847.1; -	
DR	EMBL; L10820; AAA16863.1; -	
DR	EMBL; AC018755; AAF87842.1; -	
DR	EMBL; BC005315; AAH05315.1; -	
DR	PIR; A35495; A35495.	
DR	PIR; A36309; A36309.	
DR	Genew; HGNC:3826; FPR1.	
DR	MIM; 136537; -	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PRINTS; PR00237; GPCRHHODPSN	
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.	
DR	KW Chemotaxis; Polymorphism.	
FT	DOMAIN 1 27	
FT	TRANSMEM 28 50	1 (POTENTIAL).
FT	DOMAIN 51 61	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 62 83	2 (POTENTIAL).
FT	DOMAIN 84 100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 101 121	3 (POTENTIAL).
FT	DOMAIN 122 140	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 141 162	4 (POTENTIAL).
FT	DOMAIN 163 205	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 206 226	5 (POTENTIAL).
FT	DOMAIN 227 242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 243 266	6 (POTENTIAL).
FT	DOMAIN 267 285	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 286 305	7 (POTENTIAL).
FT	DOMAIN 306 350	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 4 4	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 10 10	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DISULFID 98 176	POTENTIAL.
FT	VARIANT 101 101	L -> V.
FT	VARIANT 192 192	/FTIG=VAR_003476.
FT	VARIANT 346 346	N -> K.
FT	VARIANT 238 238	/FTIG=VAR_003477.
FT	CONFLICT 350 AA; 38401 MW; 0663EFF8267E2BD1 CRC64;	A -> E.
FT	SEQUENCE	R -> P (IN REF. 1).
SQ		
Query Match		
Best Local Similarity	68.4%; Score 1243.5; DB 1; Length 350;	
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps		
Y	1 METNFSTPLNEYEEVSYESAGVTYLRLPLVLVLTGTFVLGVNGLVIVWAGFRMTRTVT 60	: : :       : : :       : : :       : : :       : : :
Db	1 METNSSLPNTNISGGTPAVSAGYLELDITLYLFAVTFVLGVNGLVIVWAGFRMTHRTVT 60	: : :       : : :       : : :       : : :       : : :
QY	61 TICYLNIALADSFATLPFLVLSVMAGEKPFPGFLCKLIHVVDINLFSGVFLLIGRIA 120	:       :       :       :       :       :       :       :
Db	61 TISYLMNLVADECFSTLTDFPFVRMKAGHWPFPGFLCKFLTETIDINLFSGVFLLIALIA 120	:       :       :       :       :       :       :       :
QY	121 LDRCICVLHPVWAQHRTVSLAMKVIVGPWILALVTLTLPVLELTVTTIPNGDTVCTENF 180	:       :       :       :       :       :       :       :
Db	121 LDRCVCVLHPVWTQNHTVSLSAKKVIIGPWVALLTLPLVIIRVTVPGKTGTACTENF 180	:       :       :       :       :       :       :       :
QY	181 ASWGTPPERLKVAITMLTGARGIIRPVTFGSPLPMISAIVCYGLIAAKTKHKGMIKSSRPL 240	:   :    :    :    :    :    :    :    :    :    :    :    :    :    :
Db	181 SPWTDPKERINVAAMLTVRGIIIRFIIFGSAPNSIVAVSYGLIATKHKGQLIKSRPL 240	:   :    :    :    :    :    :    :    :    :    :    :    :    :    :
QY	241 RYLTVAVASFFTCWPFOLFVALLGWVWLKEMLFYCXYKIIDIIVNPTSSLAFFNSCLNMP 300	:       :       :       :       :       :       :       :
Db	241 RVLSFVAFAFFLCWSFYQVVALLIAIVRIELV-QCMYKEIGIAVDVTSALAFFNSCLNMP 299	:       :       :       :       :       :       :       :
QY	301 LVYFGQDPRERLIHSPTSLSRALSEDSAPTNDTAANSAPPAETELQA 350	:       :       :       :       :       :       :       :
Db	300 LVYFMGDQPRELIHALPASLERALTOSTSDTATNSTLPSAEVALQA 349	:       :       :       :       :       :       :       :

RESULT 13  
FMLR\_PANTR STANDARD; PRT; 346 AA.  
ID FMLR\_PANTR  
P79241:  
15-JUL-1998 (Rel. 36, Created)  
15-JUN-1998 (Rel. 36, Last sequence update)  
15-JUN-2002 (Rel. 41, Last annotation update)  
fMet-Leu-Phe receptor (FMLP receptor) (N-formyl peptide receptor)  
(FPR) (N-formylpeptide chemoattractant receptor) (Fragment).  
FPRI.  
GN  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
NCBI\_TaxID=9598;  
RN [1]  
LN  
RX MEDLINE FROM N.A.  
RP MEDLINE=96421539; PubMed=8824156;  
RA Alvarez V., Coto E., Sehen F., Gouzaiek-Koces S., Lopez-Larrea C.;  
RL "Molecular evolution of the N-formyl peptide and c5a receptors in  
non-human primates";  
IMMUNOGENETICS 44:446-452(1996).  
CC -I- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,  
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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or send an email to license@isb-sib.ch).  
-----  
EMBL; X97745; CAA66329.1; .  
DR InterPro: IPR00276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
Chemotaxis.  
KW  
NON\_TER 1  
DOMAIN <1 24  
TRANSMEM 25 47  
DOMAIN 48 58  
TRANSMEM 59 80  
DOMAIN 81 97  
TRANSMEM 98 117  
DOMAIN 119 137  
TRANSMEM 138 159  
DOMAIN 160 202  
TRANSMEM 203 223  
DOMAIN 224 239  
TRANSMEM 240 263  
DOMAIN 264 282  
TRANSMEM 283 302  
DOMAIN 303 >346  
FT CARBOHYD 1 1  
FT CARBOHYD 7 7  
FT DISULFD 95 173  
FT NON\_TER 346 346  
SEQUENCE 346 AA; 37986 MW; 97D3D7F45439BBD2 CRC64;  
  
Query Match 67.4%; Score 1225.5; DB 1; Length 346;  
Best Local Similarity 68.6%; Pred. No. 7e-64;  
Matches 238; Conservative 35; Mismatches 73; Indels 1; Gaps 1;  
  
QY 4 NFSTPLNEEVEYSAGTVLRILPLVLVGVTVLVGLNGSLVIWAGFRMTRVTTIC 63  
DB 1 NSLPTNTSGGPPAVSAGYLFDITLYLVFAVTVLVGLVGLNGSLVIWAGFRMTHTVTIS 60

QY 64 YLNALADSFATLPFLIVSMAMGEKWPFGWFLCKLHIHVVDINLFGSVFLGFIADLR 123  
 DDb 61 YLNLAADFCFTSLPFFVMKAGGHPFGWFLCKFTFTIVDINLFGSVFLGFIADLR 120  
 QY 124 CICVLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 183  
 DDb 121 CVCVLHPVMTQNHRTVSLAKKVIIGPVMALLLTLPVIRVTPGKTGTACVFNFSPW 180  
 QY 184 GGTPEERLKVAITMLTARGIRFVIGFSLPMSIVAICGLIAAKIHKMGKSSRPLRVL 243  
 DDb 181 TNDPKERINVAIAMLTVRGIIRFIIGFSAPMSIVAVSYGLIATKIHKQGLIKFSRPLRVL 240  
 QY 244 TAVVASFFICWFPQVALLGTVLWKLKEMLFYKVKYKIIDLNVPTSSLAFFNSCLNPMLYV 303  
 DDb 241 SFVAAAFCLWSPQVAVIATVRIRRELL-OGMYKEISIAVDVTSALAFFNSCLNPMLYV 299  
 QY 304 FVGQDFRERLIHSLPTSLSERALSSEDAPTNDTAANSAPPAETELQA 350  
 DDb 300 FMGQDFRERLIHSLPASLERALTEASTQTSATNSTLPSAEVALQA 346

RESULT 14  
 FMLR\_PONPY STANDARD; PRT; 346 AA.  
 AC P79235;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)  
 DE (FPR) (N-formylpeptide chemoattractant receptor) (Fragment).  
 GN FPR1.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96421539; PubMed=8824156;  
 RA Alvarez V., Coto E., Shen F., Gouzalet-Koces S., Lopez-Larrea C.;  
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in  
 RT non-human primates.";  
 RL Immunogenetics 44:446-452(1996).  
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,  
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL; X77735; CAA66319.1; -  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7tm.1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Chemotaxis.  
 FT NON\_TER 1 1  
 FT DOMAIN <1 24 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 25 47 1 (POTENTIAL).  
 FT DOMAIN 48 58 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 59 80 2 (POTENTIAL).  
 FT DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 98 118 3 (POTENTIAL).  
 FT

FT DOMAIN 119 137  
 FT TRANSMEM 138 159  
 FT DOMAIN 160 202  
 FT TRANSMEM 203 223  
 FT DOMAIN 224 239  
 FT TRANSMEM 240 263  
 FT DOMAIN 264 282  
 FT TRANSMEM 283 302  
 FT DOMAIN 303 >346  
 FT CARBOHYD 1 1  
 FT CARBOHYD 7 7  
 FT DISULFID 95 173  
 FT NON\_TER 346 346  
 SQ SEQUENCE 346 AA; 38038 MW; A012B86BAA7B315 CRC64;

Query Match 67.4%; Score 1225.5; DB 1; Length 346;  
 Best Local Similarity 68.9%; Pred. No. 7e-64;  
 Matches 239; Conservative 34; Mismatches 73; Indels 1; Gaps 1;

QY 4 NFSTPLNEYEVSYESAGYTVLRILPLVGLVGVTFVGLVGNGLVIVWAGFRMTRVTTTC 63  
 DDb 1 NSSLPTNISGGTPAVSAGYLFDIITYLVYAVTFVGLVGNGLVIVWAGFRMTRVTTTC 60  
 QY 64 YLNALADSFATLPFLIVSMAMGEKWPFGWFLCKLHIHVVDINLFGSVFLGFIADLR 123  
 DDb 61 YLNLAADFCFTSLPFFVMKAGGHPFGWFLCKFTFTIVDINLFGSVFLGFIADLR 120  
 QY 124 CICVLHPVMAQNHRTVSLAMKVIIVGFWLALVLTLPVFLFTVTPGNDTYCTFNFAW 183  
 DDb 121 CVCVLHPVMTQNHRTVSLAKKVIIGPVMALLLTLPVIRVTPGKTGTACVFNFSPW 180  
 QY 184 GGTPEERLKVAITMLTARGIRFVIGFSLPMSIVAICGLIAAKIHKMGKSSRPLRVL 243  
 DDb 181 TNDPKERIKVAIAMLTVRGIIRFIIGFSAPMSIVAVSYGLIATKIHKQGLIKFSRPLRVL 240  
 QY 244 TAVVASFFICWFPQVALLGTVLWKLKEMLFYKVKYKIIDLNVPTSSLAFFNSCLNPMLYV 303  
 DDb 241 SFVAAAFCLWSPQVAVIATVRIRRELL-OGMYKEISIAVDVTSALAFFNSCLNPMLYV 299  
 QY 304 FVGQDFRERLIHSLPTSLSERALSSEDAPTNDTAANSAPPAETELQA 350  
 DDb 300 FMGQDFRERLIHSLPASLERALTEASTQTSATNSTLPSAEVALQA 346

RESULT 15  
 FMLR\_RABIT STANDARD; PRT; 352 AA.  
 AC Q05394;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)  
 DE (FPR) (N-formylpeptide chemoattractant receptor).  
 GN FPR1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-New Zealand white; TISSUE-Neutrophils;  
 RX MEDLINE=93163563; PubMed=8432984;  
 RA Ye R.D., Quehenberger O., Thomas K.M., Navarro J., Cavanagh S.L.,  
 RA Prossnitz E.R., Cochran C.G.;  
 RT "The rabbit neutrophil N-formyl peptide receptor. cDNA cloning,  
 RT expression, and structure/function implications.";  
 RT J. Immunol. 150:1383-1394(1993)  
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,  
 CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 CC FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC

```
CC CC -!- TISSUE SPECIFICITY: NEUTROPHILS.
CC CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M94549; AAA31254.1; -.
DR PIR; A46520; A46520; GPCR_Rhodopsn.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
DR DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
DR TRANSMEM 28 50 1 (POTENTIAL).
DR DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
DR TRANSMEM 62 83 2 (POTENTIAL).
DR DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
DR TRANSMEM 101 121 3 (POTENTIAL).
DR DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
DR TRANSMEM 141 162 4 (POTENTIAL).
DR DOMAIN 163 207 EXTRACELLULAR (POTENTIAL).
DR TRANSMEM 208 228 5 (POTENTIAL).
DR DOMAIN 229 244 CYTOPLASMIC (POTENTIAL).
DR TRANSMEM 245 268 6 (POTENTIAL).
DR DOMAIN 269 287 EXTRACELLULAR (POTENTIAL).
DR TRANSMEM 288 307 7 (POTENTIAL).
DR DOMAIN 308 352 CYTOPLASMIC (POTENTIAL).
DR CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
DR CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
DR DISULFID 98 178 POTENTIAL.
DR SEQUENCE 352 AA; 38674 MW; 51DA550DAB13A091 CRC64;

Query Match 67.3%; Score 1223.5; DB 1; Length 352;
Best Local Similarity 67.7%; Pred. No. 9.3e-64;
Matches 239; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

QY 1 METNESTPLNEYEEVSYSAGTVLRILPLVVLGVTVFVLGVLGNGLVIVWAGFRMTVT 60
Db 1 MDSNASLPLNVSGGTQATPAGLVLDVDFSYLILVTVFVLGVLGNGLVIVWTFGRMTVT 60
61 TICYLNALADSFATLPELIVSNAMGEKPFGLCKLIHVVVDINLFGSVFLIGFTA 120
61 TISYLNALADSFSTLPTFFIVTALGHWPFGLCKVFETIVDINLFGSVFLIALIA 120
QY 121 LDRICVLHPVWQNRHVSLAMKVIIVGPWILALVTLPLVFLFTVTPN--GDTYCTF 178
Db 121 LDRICVLHPVWQNRHVSLAMKVIIVGPWILALVTLPLVFLFTVTPN--GDTYCTF 178
QY 179 NFASGCGTPEERLKVATMLFARGIIRVIGFSLPMSVAICYLIAAKHKMKSSR 238
Db 179 NFASGCGTPEERLKVATMLFARGIIRVIGFSLPMSVAICYLIAAKHKMKSSR 238
QY 239 PLRVLTAVVASFICFPOLVALLGTWVKEMLFYKGIIDILVNPTSSLAFFNSCLN 298
Db 239 PLRVLTAVVASFICFPOLVALLGTWVKEMLFYKGIIDILVNPTSSLAFFNSCLN 298
QY 299 PMLYVFGQDFRERLIHSIPLTSRLALSSEDSTNDTAAANSAPPAETELQAM 351
Db 299 PMLYVFGQDFRERLIHSIPLTSRLALSSEDSTNDTAAANSAPPAETELQAM 351
QY 300 PMLYVFGQDFRERLIHSIPLTSRLALSSEDSTNDTAAANSAPPAETELQAI 352
Db 300 PMLYVFGQDFRERLIHSIPLTSRLALSSEDSTNDTAAANSAPPAETELQAI 352
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Search completed: December 16, 2002, 17:18:28  
Job time : 16 secs







DE N-formylpeptide receptor-like 4.  
GN FPR-RS4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98390190; PubMed=9722950;  
RA Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;  
RT "Differential expansion of the N-formylpeptide receptor gene cluster  
in human and mouse."  
RL Genomics 51:270-276(1998).  
DR EMBL: AF071182; AAC34587.1; -.  
DR MGD; MGI:1278317; Fpr-rs4. GPCR\_Rhodpsn.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO1559; DUFFYANTIGEN.  
DR PRINTS; PRO0237; GPCR\_Rhodopsin.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_FL\_1; UNKNOWN\_1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_FL\_2; 1.  
DR Receptor.  
SQ SEQUENCE 323 AA; 36299 MW; CC90EC09B4725036 CRC64;  
Query Match 61.0%; Score 1107.5; DB 11; Length 323;  
Best Local Similarity 65.5%; Pred. No. 2.1e-88;  
Matches 215; Conservative 39; Mismatches 69; Indels 5; Gaps 1;  
QY 1 MEVNFSTPLNEYEEVYESAGYTVLRILPLVVLGVTVFVLGVLGNGLVWVAGFRMTRVT 60  
Db 1 MEVNISPLNGSEVVFYDSTSSVLSLWLFITFVLGVLGNGLVWVAGFQMAHTVT 60  
QY 61 TICVNLALADFSFATLPLPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120  
Db 61 TVSYLNALSDLSFMTPLPHIHSVMRGKWLFGWFLCKLVHIANINLFSVFLITLIA 120  
QY 121 LDRICVLPHPVAQNHRVTSVLAQVWILALVTLVPVFLFTVTTPNGDTYCFNF 180  
Db 121 MDRICVLPVPSQNHRTSVLSARVVLGAWIFALLTLPHFLFTVTRDARGDYCISKF 180  
QY 181 ASNGGTPEERLKVATMTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKMKSRPL 240  
Db 181 ESWVATSEOLKMSVTAATAGSIINFTIGFSPMSFTAICYGLMAAKICRRGFVNSSRPL 240  
QY 241 RVLTAVVASFICWFFPQLVALLGTWVKEMLFYGYKIIDILVNPFTSSLAFFNSCLNPM 300  
Db 241 RVLTAVVASFICWFFPQLVALLGNIFNETL-----SIHMLVNPANTLASFNCLNPI 295  
QY 301 LYFVVGQDFRERLIHSLPTSLERALSSED 328  
Db 296 LYFVLGQDFRDLIYSYASLERALSRED 323  
RESULT 5  
Q9QW9 PRELIMINARY; PRT; 475 AA.  
AC Q9QW9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anaphylatoxin C3a receptor.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=SPLEEN;  
RX MEDLINE=98414293; PubMed=9743361;  
RA Fukuoaka Y., Ember J.A., Hugli T.E.;  
RT "Molecular cloning of two isoforms of the guinea pig C3a anaphylatoxin  
receptor: alternative splicing in the large extracellular loop."  
RL J. Immunol. 161:2977-2984(1998).

DR EMBL: U86378; AAC36503.1; -.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCR\_Rhodopsin.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_FL\_1; UNKNOWN\_1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_FL\_2; 1.  
DR Receptor.  
SQ SEQUENCE 475 AA; 53528 MW; 2C2C4D6C02170726 CRC64;  
Query Match 30.2%; Score 549.5; DB 11; Length 475;  
Best Local Similarity 28.8%; Pred. No. 1e-39;  
Matches 136; Conservative 61; Mismatches 104; Indels 171; Gaps 10;  
QY 2 ETNFSTPLNEYEEVYESAGYTVLRILPLVVLGVTVFVLGVLGNGLVWVAGFRMTRVT 61  
Db 7 ETN-STGLHLEPQYQPET-----ILAMAILGLTFLVGLPGNLVWVAGLKMRRVTNT 58  
QY 62 ICVNLALADFSFATLPLPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL 121  
Db 59 VWFLHLTVADFVCCLSLPSMAHLALRGYPYGEILCKFTPTVIIFNMFASVFLITLISL 118  
QY 122 DRICVLPHPVAQNHRVTSVLAQVWILALVTLVPVFLFTVTTPNGDTYCFNF 181  
Db 119 DRCLMVLKPIWQNHNRVTSVLAQVWILALVTLVPVFLFTVTTPNGDTYCFNF 177  
QY 182 -----SWG-GTP----- 187  
Db 178 PGSFYLDYAYDRWAGYGTDPDPIVQLPGEMHRSDFSTQDGPWNSVTTLYSQTSSQR 237  
QY 188 --BERLKVAITMTARG----- 202  
Db 238 PSEDSFMDSAKLSGQKYYVDVPLTNLCGLPMEENTNTLHNAAFSLSSDLVSNATQK 297  
QY 203 -----IIRFVIGFSLPMSIVAICYGLIAAKIHKMKSRPL 231  
Db 298 LSTPEPQDFWDDLSPTFHEVTRPLKLVITFTRVLVGLLPMIIVACVTLIIFRMRRA 357  
QY 232 GMKKS-SRPLRVLTAVVASFICWFFPQLVALLGTWVKEMLFYGYKIIDILVNPFTSS 288  
Db 358 RVKSNWNLKHLAMVVVTFIICWAPYHV-----FGVLIIFINPESRV 400  
QY 289 -----SLAFNSCLNPMLYVVGQDFRERLIHSLPTSLERALSSED 328  
Db 401 GAALLSDWHSVIALASANSFCNPFYALLGLRKRVRQSMKKGLEAASED 452  
RESULT 6  
Q95LH1 PRELIMINARY; PRT; 355 AA.  
AC Q95LH1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE G protein-coupled receptor 1.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wade-Evans A.M., Javan C., Russell J., Jenkins A.;  
RT "Cloning and sequencing of simian G-protein coupled receptors, which  
may function as SIV/SHIV co-receptors, from cynomolgus macaque  
PBMCs."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF292382; AAK97052.1; -.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECP\_FL\_2; 1.  
DR Receptor.  
SQ SEQUENCE 355 AA; 41370 MW; 1DD4E1BE9CAC525C CRC64;

Query Match 27.5%; Score 500; DB 6; Length 355;  
Best Local Similarity 33.08; Pred. No. 1.5e-35;  
Matches 114; Conservative 69; Mismatches 132; Indels 30; Gaps 7;

QY 1 METNFTPLNEEYVS-----ESAGTIVLRILPLVLGVTFVLGVLNGLVI 48  
DB 1 MEDLEETLFEFENYSYALDYSLDESLEEKVQGVHWSLVLYCLSFVLGPGNAIVI 60

QY 49 WVAGFRWTRVTTCYLNALADSFATLPPLVSMAMGKWPFGWFLCKLIHIVVDIN 108  
DB 61 WFTGFKWRTVSTLWFLNALADHIFLFLPLYSYVVMNFHWPFGIWLCKANSFTAOLN 120

QY 109 LFGSVLIGETALDCICVLHPVMAQNHRTVSLAMKVIIVGVWILALVTLPLVFLFTVT 168  
DB 121 MFASVFFTVISLDHYIHLHPVSHRRTLKNSLVIIIFILWLASLGGPALYFRDTVE 180

QY 169 IPNGDTYCTFNFSWGGTPEERLKVATMLTARGI--IRFVIGFSLPMSIVAICYGLIAA 226  
DB 181 F-NHNTLCYNF-----QKHDPLAVIRHHVLTWVKYIVGYLFLPLTMSICYLCIL 231

QY 227 KHKMGMTKSRPLRLVLTAVVASFFICWFPQVLVALLGTVMKEMFLGYGKYK--IIDLIV 284  
DB 232 KVKRSILISSRHEWFTILAVVAFVVCVTPYHLF----SIW-ELTIHNSYSHRVMAQGI 286

QY 285 NPTSLAFENCLNPLVYFVGQDFRERLIHSLPTSLERALSDDS 329  
DB 287 PLSTGLAFENCLNPLVYFVGQDFRERLIHSLPTSLERALSDDS 331

RESULT 7  
Q9PVY7 PRELIMINARY; PRT; 359 AA.

AC Q9PVY7; 2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Angiotensin receptor.  
OS Anguilla anguilla (European freshwater eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.  
OX NCBI\_TaxID=7936;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tran Van Chuoi M., Dolphin C.T., Barker S., Clark A.J., Vinson G.P.;  
RT "Molecular cloning and characterization of the cDNA encoding the  
angiotensin II receptor of european eel Anguilla anguilla";  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AJ005132; CAB40835.1; -.  
DR HSSP; P34996; 1DDD.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR000130; 2n\_MTPeptidase.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
SQ SEQUENCE 359 AA; 39997 MW; 053726AE827C271 CRC64;

Query Match 25.2%; Score 457.5; DB 13; Length 359;  
Best Local Similarity 34.7%; Pred. No. 7.6e-32;  
Matches 119; Conservative 59; Mismatches 126; Indels 39; Gaps 10;

QY 24 VLRLPLVWLGTVFVLGVLGVLGVIWA-GFRWTRVTTCYLNALADSFATLPFLI 82  
DB 25 IYTLIP-VVYGCNFIIVIGVSMVAVIYCYMKIKTAVNFVLNLAISDLTFLITLPMA 83

QY 83 VSMAMGKWPFGWFLCKLIHIVVDINLFGSVFLIGETALDCICVLHPVMAQNHRTVSLA 142

DB 84 TTTAGYNNPFGGLCKASAGITITFNLTSTIFFLSLSDIRLYALHVPVRSQRRTVVA 143  
QY 143 MKVIVGPWILALVTLPLVFLFTVTI--PNGDTYCTFNFSWGGTPEERLKVATMLTA 200  
DB 144 RITCVLIWAFAPLSPALSDRQVFTINHPN-TTVC-----GTLDKHELS--HVLVA 192

QY 201 RGIIRFVIGFSLPMSIVAICYGLIAAKHKKGMKSSRP-----LRVLTAVVASFFICWF 255  
DB 193 IGLMSVGLTIPFVITVTCYCLIGRALLARRVQSSSRGDEVQLMLAAVVAFLFCWV 252

QY 256 PFQVLVALLGTV-WKEMLFYKIKTIIDLVNPTSSLAENCLNPLVYFVGQDFRERLI 314  
DB 253 PHQIFHMHVLAHLKVIENCPDLDIIDTALPFTICIAVFNSCMNPILYGFVGRNRRLL 312

QY 315 -----HSLP-----TSLERALSDDSAPTNDTAANS 339  
DB 313 RLLRCGPGSAARHSHPSLTTRKMSILSYRASETLRLTSGKAASS 355

RESULT 8  
Q93247 PRELIMINARY; PRT; 353 AA.

AC Q93247;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE CXCR4.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-99367403; PubMed-10436187;  
RA Fujiki K., Shin D., Nakao M., Yano T.;  
RT "Molecular cloning of carp (Cyprinus carpio) CC chemokine, CXCR4,  
a chemokine receptor, allograft inflammatory factor-1, and natural  
killer cell enhancing factor by use of suppression subtractive  
hybridization";  
RL Immunogenetics 49:909-914(1999).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AB012310; BA332797.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR01558; CHEMOKINER11.  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PRINTS; PR01568; LYMPHOTACTNR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;

Query Match 23.8%; Score 433; DB 13; Length 353;  
Best Local Similarity 31.5%; Pred. No. 1e-29;  
Matches 112; Conservative 66; Mismatches 114; Indels 64; Gaps 13;

QY 10 NEVEEVYESAGYTVLRILPLVWLGTVFVLGVLGVLGVIWA-GF-RWTRVTTCYLNLA 68  
DB 32 NDFQKI-----FLP-VVYGIIFVLGIIGLVLGVLGVLGVLGVLGVLGVLGVLGVL 79

QY 69 LADFSFTATLPFLIVSMAMGKWPFGWFLCKLIHIVVDINLFGSVFLIGETALDCICVL 128  
DB 80 IADLLFVLTPFWAVDAASG--WHFEGFLCVTVNNIYTLNLYSSVLIILAFISLDRLYAV 137

QY 129 HPVMAQNHRTVSLAMKVI-VGPWILALVTLPLVFLFTVTIPNGDTYCTFNFSWGGT 187  
DB 138 RATNSQNFRRY-LAEKVIYLGWLPASLLTPDLVF-AKVHDTGMNTICELTYPLQGTN- 194

QY 188 EERLKVAITMLTARGIIRF--VIGFSLPMSIVAICYGLIAAKIHK--KGMIKSRPLRV 242

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Db 195 -----VKAVERFQHFVGFLLPGLIILTCYCIILSKSKSGQALRKALKT 243
QY 243 LTAVVASFFICWFQFQVALLGTV-----WLKEMLFYKYKIIDIILVNPTS 288
Db 244 TVIILLCFFICWPCAGILVDITMLNLSHTCFLEQGLKWIFF-----TE 291
QY 289 SLAFNSCLNMLVVFVGGQDFRRLIHL---PTSLERALSSEDSAPTNDTAANSAS 341
Db 292 ALAYFHCLNPLILYAFGLVFKSKARNALSISRSSHMLTKKRGPISSVSTES 347

RESULT 9
ID Q9GLN9 PRELIMINARY; PRT; 359 AA.
AC Q9GLN9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Angiotensin II type-1 receptor.
GN AGRI1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469400; Pubmed=11013071;
RA DuFour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunemaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin-angiotensin system.";
RL Genomics 69:14-26(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF193445; AAG28410.1; -.
DR HSSP; P34996; 1DDO.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41033 MW; 266133A7A3E911A6 CRC64;

Query Match 23.5%; Score 427.5; DB 6; Length 359;
Best Local Similarity 31.0%; Pred. No. 3.1e-29;
Matches 103; Conservative 69; Mismatches 123; Indels 37; Gaps 9;

QY 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYICLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLAALADLCFLLLPLWAVYTAMEYRWPF 96
QY 94 GWFLCKLHIHVVINDLFGSVFLIGFIALDRICVLPVWQNHRTVSLAMKVIVGWPWLA 153
Db 97 GNYLCKIASASVSNLYASVELLCTSLDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
QY 154 LVLPVLPFLFTVTIPNGD--TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGSL 212
Db 157 GLASLPALIHNRNVEFIENTITVCAFYHESQNST----LPIGL-----GLTKNIGLFL 206
QY 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTSYTLIWLKAKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
QY 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNPLVVFVGGQDFR---RLIHLSP 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKFKKRYFLQLLKVIP 321
QY 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSKMTSLSYRSDNVSSSTKKPA 353

QY 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYICLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLAALADLCFLLLPLWAVYTAMEYRWPF 96
QY 94 GWFLCKLHIHVVINDLFGSVFLIGFIALDRICVLPVWQNHRTVSLAMKVIVGWPWLA 153
Db 97 GNYLCKIASASVSNLYASVELLCTSLDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
QY 154 LVLPVLPFLFTVTIPNGD--TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGSL 212
Db 157 GLASLPALIHNRNVEFIENTITVCAFYHESQNST----LPIGL-----GLTKNIGLFL 206
QY 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTSYTLIWLKAKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
QY 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNPLVVFVGGQDFR---RLIHLSP 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKFKKRYFLQLLKVIP 321
QY 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSKMTSLSYRSDNVSSSTKKPA 353

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RESULT 10
Q8TBK4
ID Q8TBK4 PRELIMINARY; PRT; 359 AA.
AC Q8TBK4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Angiotensin receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022447; AAH22447.1; -.
KW Receptor.
SQ SEQUENCE 359 AA; 41087 MW; AF90BE7F21E911BA CRC64;

Query Match 23.5%; Score 426.5; DB 4; Length 359;
Best Local Similarity 31.0%; Pred. No. 3.8e-29;
Matches 103; Conservative 68; Mismatches 124; Indels 37; Gaps 9;

QY 35 VTFVLGVLGGLVIVVAGFRM-TRVTTCYICLNALADFSFATLPLFLIVSMAMGEKWP 93
Db 37 IIFVVGIFGNSLVIVYFYMKLTVASVFLNLAALADLCFLLLPLWAVYTAMEYRWPF 96
QY 94 GWFLCKLHIHVVINDLFGSVFLIGFIALDRICVLPVWQNHRTVSLAMKVIVGWPWLA 153
Db 97 GNYLCKIASASVSNLYASVELLCTSLDRYLAIVHPMKSLRRTMLVAKVTCIIWLLA 156
QY 154 LVLPVLPFLFTVTIPNGD--TYCTFNPSWGGTPEERLKVATMLTARGIIRFVIGSL 212
Db 157 GLASLPALIHNRNVEFIENTITVCAFYHESQNST----LPIGL-----GLTKNIGLFL 206
QY 213 PMSIVAICYGLIAAKIHKKGKSRP-----LRVLTAVASFFICWFQFQVALLGTVW 267
Db 207 PFLIILTSYTLIWLKAKAYEQKNKPRNDDIFKIIAIVLFFFSWIPHQIFTLFDV-- 264
QY 268 LKEMLFYGYKYK-----IIDILVNPTSLAFNSCLNPLVVFVGGQDFR---RLIHLSP 318
Db 265 ---LIQLGIIRDCTADIVDTAMPITICIAFNCLNPLFVGLGKFKKRYFLQLLKVIP 321
QY 319 -----TSLERALSSEDSAPTNDTAANSASPPA 344
Db 322 PKAKSHSNLSKMTSLSYRSDNVSSSTKKPA 353

RESULT 11
Q9EPP3
ID Q9EPP3 PRELIMINARY; PRT; 359 AA.
AC Q9EPP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
GN ATI.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GALL BLADDER;
RA Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.;
RT "Isolation of Angiotensin I from human hemofiltrate as a potent
RT modulator of KATP channels.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ301623; CAC21550.1; -.

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QY 85 MAMGEKWPFGWFLCKLIHIVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 93 AV--ANNYFGNFCCKAVHVIYTVNLYSSVLLIAFISLDRLYLAIVHATNSQKPKRL-LAEK 149
QY 145 VI-VGPMILALVTLPLVFLFTVT-----IPNGDTYCTFNFSWGGTPEERLKV 193
DB 150 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRFPNDLVVVVFQF----- 197
QY 194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKGMKISRRLRVLTAVASFFI 252
DB 198 -----HIMVGLILPGVILSCYIIISKLSHSGHQK-RKALKTTVILIAFFA 245
QY 253 CWPFQVALLGVTLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPLVYFVG 306
DB 246 CWLPYVIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 301
QY 307 QDFRERLIHSLPTSLEALS 326
DB 302 AKFKTSAQHAL-TSVSRGSS 320
RESULT 14
Q9TSQ8 PRELIMINARY; PRT; 352 AA.
AC Q9TSQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE G-protein coupled receptor.
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Holtkamp N., Baier M., Warner A.;
RT "CXCR4 from African green monkey.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF019378; AD01638.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR01558; CHEMOKINER11.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 39624 MW; F240B686D6B368F CRC64;

Query Match 23.2%; Score 421.5; DB 6; Length 352;
Best Local Similarity 33.1%; Pred. No. 1e-28;
Matches 106; Conservative 56; Mismatches 107; Indels 51; Gaps 11;

QY 26 RILPLVVLGVTVFVLGVLGNGLVIVVAGF-RMTRVTTCVILNLAALDFSTATLPFLIVS 84
DB 38 RILPLTIYSIIFLTGIVGNGLVILVMGYOKKLSMTDKYRLHLSVDALLFVITLPFWAVD 97
QY 85 MAMGEKWPFGWFLCKLIHIVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 98 AV--ANNYFGNFCCKAVHVIYTVNLYSSVLLIAFISLDRLYLAIVHATNSQKPKRL-LAEK 154
QY 145 VI-VGPMILALVTLPLVFLFTVT-----IPNGDTYCTFNFSWGGTPEERLKV 193
DB 155 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRFPNDLVVVVFQF----- 202
QY 194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKGMKISRRLRVLTAVASFFI 252

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DB 203 -----HIMVGLILPGVILSCYIIISKLSHSGHQK-RKALKTTVILIAFFA 250
QY 253 CWPFQVALLGVTLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPLVYFVG 306
DB 251 CWLPYVIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 306
QY 307 QDFRERLIHSLPTSLEALS 326
DB 307 AKFKTSAQHAL-TSVSRGSS 325
RESULT 15
Q9MZP3 PRELIMINARY; PRT; 347 AA.
AC Q9MZP3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chemokine receptor CXCR4 (Fragment).
GN CXCR4.
OS Presbytis entellus (Hanuman langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=9574;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172220; AAF89340.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR01558; CHEMOKINER11.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39145 MW; E96B660F1541515C CRC64;

Query Match 23.2%; Score 421; DB 6; Length 347;
Best Local Similarity 31.8%; Pred. No. 1.1e-28;
Matches 110; Conservative 59; Mismatches 115; Indels 62; Gaps 12;

QY 26 RILPLVVLGVTVFVLGVLGNGLVIVVAGF-RMTRVTTCVILNLAALDFSTATLPFLIVS 84
DB 33 RILPLTIYSIIFLTGIVGNGLVILVMGYOKKLSMTDKYRLHLSVDALLFVITLPFWAVD 92
QY 85 MAMGEKWPFGWFLCKLIHIVDINLFGSVFLIGFIALDRICVILHPWAQNHRTVSLAMK 144
DB 93 AV--ANNYFGNFCCKAVHVIYTVNLYSSVLLIAFISLDRLYLAIVHATNSQKPKRL-LAEK 149
QY 145 VI-VGPMILALVTLPLVFLFTVT-----IPNGDTYCTFNFSWGGTPEERLKV 193
DB 150 VVYGVWIPALLTIPDFIFASVSEADDRFCDFRFPNDLVVVVFQF----- 197
QY 194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKGMKISRRLRVLTAVASFFI 252
DB 198 -----HIMVGLILPGVILSCYIIISKLSHSGHQK-RKALKTTVILIAFFA 245
QY 253 CWPFQVALLGVTLKEMLFY-----KYKIIDLINVTSSLAFFNSCLNPLVYFVG 306
DB 246 CWLPYVIGISIDSFILLEIKQCEPENTVHKWISI-----TEALAFPHCCNLPILYAFLG 301
QY 307 QDFRERLIHSLPTSLEALS-----EDSAPTNDTAANSAS 341

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Db 302 AKFTSAQHAI-TSVRGSSILKILSKRGCHSVSTESSESSHS 346

Search completed: December 16, 2002, 17:19:30  
Job time : 36 secs





QY 61 TICYNLALADSFATLPFLIVSLAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TISYNLAVADECFSTLPFFMVRKAMGHPFGWFLCKLEFETIVDINLFGSVFLIALIA 120  
QY 121 LDRICVILHPVWQAQNRHTVSLAMKIVIVGFWILALVLTLPVFLFATVTPNGDTCYTFNF 180  
DB 121 LDRICVILHPVWQAQNRHTVSLAMKIVIVGFWILALVLTLPVFLFATVTPNGDTCYTFNF 180  
QY 181 ASWGCTPERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
DB 181 SPWTNDPNERIKVAVAMLTVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
QY 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLNVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLNVNPTSSLAFFNSCLNPM 300  
QY 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349  
DB 300 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349

## RESULT 2

US-08-430-286A-8  
; Sequence 8, Application US/08430286A  
; Patent No. 6225080

## GENERAL INFORMATION:

; APPLICANT: Unl, George R.  
; APPLICANT: Eppler, C. Mark  
; APPLICANT: Wang, Jai-Bel  
; TITLE OF INVENTION: Mu-Subtype Opioid Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darby & Darby PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10022

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/430, 286A  
; FILING DATE: 28-APR-1995  
; CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

; NAME: Robinson, Joseph R.  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 0846/1A843-US  
; TELEPHONE: 212-527-7700  
; TELEFAX: 212-753-6237  
; TELEX: 236687

## INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: F-PEP  
; US-08-430-286A-8

Query Match 68.3%; Score 1240.5; DB 4; Length 350;  
Best Local Similarity 68.6%; Pred. No. 1.4e-84;  
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFTPLNEYEVSYESAGYTVLRILPLVLVGLVGLNGLVWAGFRMTRVT 60

DB 1 METNFTPLNEYEVSYESAGYTVLRILPLVLVGLVGLNGLVWAGFRMTRVT 60  
QY 61 TICYNLALADSFATLPFLIVSLAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTA 120  
DB 61 TISYNLAVADECFSTLPFFMVRKAMGHPFGWFLCKLEFETIVDINLFGSVFLIALIA 120  
QY 121 LDRICVILHPVWQAQNRHTVSLAMKIVIVGFWILALVLTLPVFLFATVTPNGDTCYTFNF 180  
DB 121 LDRICVILHPVWQAQNRHTVSLAMKIVIVGFWILALVLTLPVFLFATVTPNGDTCYTFNF 180  
QY 181 ASWGCTPERLKVATMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
DB 181 SPWTNDPNERIKVAVAMLTVRGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240  
QY 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLNVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTAVASFFICWPFQVALLGVWLMKEMLFYCKYKIIDLNVNPTSSLAFFNSCLNPM 300  
QY 301 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349  
DB 300 LYVFGQDFRERLIHALPASLERALTEDSTQTSATNSTLPSAEVALQA 349

## RESULT 3

US-08-458-970A-10  
; Sequence 10, Application US/08458970A  
; Patent No. 5861272

## GENERAL INFORMATION:

; APPLICANT: LI, ET AL.  
; TITLE OF INVENTION: C5a Receptor  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068

## COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA: US/08/458, 970A  
; FILING DATE: June 2, 1995  
; CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/09234  
; FILING DATE: 16 AUG 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744

## INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 364 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-970A-10

Query Match 64.6%; Score 1174.5; DB 2; Length 364;  
Best Local Similarity 64.6%; Pred. No. 1.1e-79;  
Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

QY 1 METNFTPLNEYE-----EVSYESAGYTVLRILPLVLVGLVGLNGLVWAG 52

Db 1 MTNLSLLMKNKSAVNLMMVSGTSQSVAGYIVLDVFSGLIFAVTVLGVGLNGLVIWAG 60  
Qy 53 FRMTFTVTTCYNLALADFSFATLPFLIVSMAMGKWPFGWFLCKLIHIVVDINLFGS 112  
Db 61 FRMKTHTTISYLNLAIDFCFTSTLPFYIASVMGHHWPFGEWCKFTYTVIDINLFGS 120  
Qy 113 VFLIGFIALDRCCICVLHPVMAQNHRTVSLAMKVIIVGPHILALVLPVLELFTVTPN- 171  
Db 121 VFLIALIALDRCCICVLHPVMAQNHRTVSLAMKVIIVGPHILALVLPVLELFTVTPN- 178  
Qy 172 ---GDTYCTFNFAWSGCTPPEERLKVAITMLTARIIIFVIGFSPMSIVAICYGLIAAK 227  
Db 179 RLGPCKTACTDFEPTWKDPVEKRVAVTMLTVRGIIIFIGFSPMSIVAICYGLITK 238  
Qy 228 IHKGMKSSRLRVLTAVASFFFCWPPFQVALLGVTKMLFYGYKYKIIDLNVPT 287  
Db 239 IHRQGLIKSSRLRVLTAVASFFFCWPPFQVALLGVTKMLFYGYKYKIIDLNVPT 297  
Qy 288 SSLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALSSEDAPTNDTAAN---SASPPA 344  
Db 298 SPLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALSSEDAPTNDTAAN---SASPPA 357  
Qy 345 ETELQAM 351  
Db 358 ENTLNAM 364

RESULT 4  
US-08-118-270-34  
; Sequence 34, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 315 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-118-270-34

Query Match 61.5%; Score 1117; DB 1; Length 315;  
Best Local Similarity 67.3%; Pred. No. 1.7e-75;  
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;  
Qy 27 ILPLVVLGVTVFVLGVGLNGLVIWAGFMRTRVTTTCYNLALADFSFATLPFLIVSMA 86  
Db 1 IITLVFAVRVFLGVGLNGLVIWAGFMRTHVTITISYLNLAADFCFTSTLPFFWVRLG 60  
Qy 87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCCICVLHPVMAQNHRTVSLAMKYI 146  
Db 61 ---HWPFGEWFLCKFTYTVIDINLFGSVFLIGFIALDRCCICVLHPVMAQNHRTVSLAMKYI 117  
Qy 147 VCPWILALVLTLPVLELFTVTPNPGDITVCTFNFAWSGCTPPEERLKVAITMLTARGIIRF 206  
Db 118 IGPWMAALLTTLTVIRVTIVPGKTGVACTFNFSPTNDPKERINAVAMLTVRGIIRF 177  
Qy 207 VIGFSLPMSIVAICYGLIAAKIHKGMKSSRLRVLTAVASFFFCWPPFQVALLGVTK 266  
Db 178 IIGFSAFMSIVAICYGLIAAKI---IKSSRLRVLTAVASFFFCWPPFQVALLGVTK 232  
Qy 267 WUKEMLFYGYKYKIIDLNVPTSLAFNSCLNPLMVLVFGQDFRERLIHSLPTSLERALS 326  
Db 233 RIRELL-QCMYKEIGIAVDVTSIAIAFNSCLNP-LYVFMGQDFRERLIHALPASLERALT 290  
Qy 327 EDSAPTNDTAANSASPPAETELQA 350  
Db 291 EDSTQTSATNTSLPSAEVALQA 314  
RESULT 5  
PCT-US93-08528-34  
; Sequence 34, Application PC/TUS9308528  
; GENERAL INFORMATION:  
; APPLICANT: New York University  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08528  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 315 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-08528-34

Query Match

61.5%; Score 1117; DB 5; Length 315;

Best Local Similarity 67.3%; Pred: No. 1.7e-75;  
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;

QY 27 ILPLVLGVTVFLVGLNGVLVWVAGFRMRTVTTCYLNALADFSTATPLLIYSMA 86  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 1 IITLVFAVRFVLVGLNGVLVWVAGFRMHTVTTSYLNLAADFSTSLPFMWRLG 60  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 87 MGKWPGEFLCKLIHLVINDLFGSVFLGFIAGFDALDRCICVLHPVWQNHRTVSLAMKVI 146  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 61 ---HWPFGEFLCKFLFTIVDINLFGSVFLIALIALDRCVCLHPVWQNHRTVSLAKKVI 117  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 147 VGPWIALVLTLPVFLPLTVTTPNGDTCYCTFNPFASNGCTPEERLKYAITMLTARGIIRF 206  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 118 IGSFWALLTLPLVIRKVTIVPGKTVGTVACTFNFSPMTNDPKERINAVAMLTVRGIIRF 177  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 207 VIGFSLPMSIVAICYGLIAAKIHKKGMKISSRPLRVLTAVVASFFICWFPPOLVALLGTV 266  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 178 IIGFSAPMSIVASYGLIAYKI-----IKSSRPLRVLSFVAAAFCLWSPQVVALTATV 232  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 267 WLKEMFLPYGKIIDLIVNPTSSLAFFNSCLNPLMYVFGODFRERLIHSLPTSLEIALS 326  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 233 RIRELL-QGMKEIGIADVTSATAFNSCLNP-LYVFMGQDFRERLIHALPASLERALT 290  
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

QY 327 EDSAPTNDTAANSASPPAETELQA 350  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | : |  
Db 291 EDSTQTSDTATNSTPLSAEVALQA 314  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

RESULT 6  
US-08-513-9748-348  
; Sequence 348, Application US/08513974B  
; Patent No. 6114139  
; GENERAL INFORMATION:  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Hosoya, Masaki  
; APPLICANT: Fujii, Ryo  
; APPLICANT: Ohtsaki, Tetsuya  
; APPLICANT: Fukusumi, Shoji  
; APPLICANT: Ohgi, Kazuhiro  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994

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; APPLICATION NUMBER: US/08/458,970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-970A-9

Query Match      28.2%; Score 513; DB 2; Length 350;
Best Local Similarity 33.6%; Pred. No. 7.3e-31;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

QY 4 NESTP-LNEYER-----VSYESAGYVLRILPLVVLGVTFVLGVLGNGLVIWVAGF 53
DB 5 NYTTPDGHYDDKDTLDLNTVPDKTSNLRVPDILALVIFAVFLVGLGNALVWVMTAF 64

QY 54 RMTRVTTICYNLALADFSFATIPELIVSNMAGEKWPFGWFLCKLIHIVVDINLFGSV 113
DB 65 EAKRTINAIWFLNLAADFSLCLAPILFTSIVQHHHPFPGAACSLILSLILLNMYASI 124

QY 114 FLIGTALDRCTICVLHPVMAQNHRVTSAMKVIVGFWIILALVLTPLVFLFTVTVTPNGD 173
DB 125 LLLATISADRELVLKPIWCQNFRCAGLAWIACAVAGLALLTIPSLFYRVV-----RE 179

QY 174 TY-----CTFNFASWGTPPEERLKVATMLTARIIIFVIGFSIPMSIVAICYGLIAAK 227
DB 180 EYFPKVLGCVDYSH-----DKRRERAV-----AIVRLVGLFWPLLTLCITYFILLR 228

QY 228 IHKGMKISSRPLRVLTAVASFFCWFQFOLVALLGTWVKEMLFYGYKIKIILVNPT 287
DB 229 TWSRRATSTKLVVAVASFFFLFWLPYQVTGM-----MSFLEPSSFTLLLNKL 281

QY 288 SSL-----AFFNSCLNPMILYVFQDFRERLIHSLPTSLSRALSEDA-----PTND 334
DB 282 DSLCVSFAYINCCINPIIYVAGQGFQGLRKLKSLPSLLRNVLTEESVYRESKSFTRSTVD 341

QY 335 TAA 337
DB 342 TMA 344

RESULT 8
US-08-876-874-2
; Sequence 2, Application US/08876874
; Patent No. 5942405
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert
; APPLICANT: Bergsma, Derek
; APPLICANT: Foley, James
; APPLICANT: Kumar, Chandrika
; APPLICANT: Sarau, Henry
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
; METHODS USING C3A RECEPTOR AND C3A
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
```

```
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,874
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,627
; FILING DATE: 16-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-876-874-2

Query Match      28.0%; Score 508.5; DB 2; Length 482;
Best Local Similarity 26.6%; Pred. No. 2.2e-30;
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 EN-----ESTPLNEEVEESYESAGYVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRWTR 57
DB 7 ENSTDLSQWNEPVPV-----ILSMVILSLFTLLGLPGNLVWVAGLKMQR 54

QY 58 TTTTCYLMALADFSFATPLPLIVSMAGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
DB 55 TWNTWFLHLLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSLIIVLNFASFVLLT 114

QY 118 FTALDRCTICVLHPVMAQNHRVTSAMKVIVGFWIILALVLTPLVFLFTVTVTPNGDYCT 177
DB 115 AISLDRCLVYFKPIWCQNHNRVGMAGSICGCIWVAVCMCIPVYVYREIFTTNNHR-CG 173

QY 178 ENFA-----SW-----183
DB 174 YKFGSSSLDYPDFYGDPLNRSLENIIVQPGEMNDRLDPSSFQTNHDPWTVPTVFQPT 233

QY 184 -----GGTPEE-----R 190

DB 234 FORPSADSLPGSARLTSQLYSNVFKPADVVPKIPSGFPFIEDHETSPLDNSDAFLSTH 293

QY 191 LKV-----AITMLTARGIRFIRFVIGSLPMSIYA 218
DB 294 LKLPFSASSNSFESELPQGFQDYNNLQGTDDDDQVPTPLVAITITRLVVGFLPSVIMI 353

QY 219 ICYGLIAAKIHKGMKIS-SRPLRVLTAVASFFCWFQFOLVALLGTWVKEMLFYGYK 277
DB 354 ACYSFIVFMQRGRFAKSQSKTFRVAVVAVFLVCWTPYHI-----F 396

QY 278 KIIDLIVNPTS-----SLAPFNSCLNPMILYVFQDFRERLIHSLPTSLSR 323
DB 397 GVLSTLTPETPLGKTLMSDHWCIALASANSCLNPMILYVALLGKDFRKARSIQIGILEA 456

QY 324 ALSD-----SAPTNDTANSAS 341
DB 457 AFSEELTRSTHCPSCNNVISERN 479

RESULT 9
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Query Match 27.8%; Score 504.5; DB 3; Length 395;  
Best Local Similarity 34.0%; Pred. No. 3.5e-30;  
Matches 119; Conservative 75; Mismatches 129; Indels 27; Gaps 6;

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;
; STRANDEDNESS: unknown
;
; TOPOLOGY: unknown
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-09-480-784-6

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QY	13	EEVS-YESAGYTVLRL--PLVVLGVTVTVGLVGNGLVWVAGFRTMTVTTTCYNLNA	68
Db	15	EQMSRLQSHSNTSIRYIDHAAVLHGLSLLGVENGVLFFVVGCRMTQVTVTTVTVWLHLA	74
QY	69	LADFSFATLPELLIVSMWGEKPFGEFLCKLIHVVDINLFGSVFLIGFIALDRCICVYL	128
Db	75	LSDLLASASUPPTYFLAVGHSWELETGTCCKLHSSIFFLNMFFASGFLLSAIDRLCQVW	134
QY	129	HPVWQNHRTVSLAMKVIYGPMTLALVLPVFLFTVTTIPNGDPYCFNFEASMGGTPE	188
Db	135	RPVWQNHRTVAAAHKVCVLVNALAVLTPYFVPRDTISRLDGRIMCYYNVLLNPGP-	193
QY	189	ERUKVAITMLTARGIITFVIGFSLPMSIVAICYGLIAAKIHKKGMTKTSRRLRVITAVVA	248
Db	194	DRDATCSRQAALAVSKFLAFIAVPLAIITASSHAAYSLRLQHRGRRRPGRFVRLAAVVA	253
QY	249	SFFICWFEPQVALL-----GTWLKEMLFYGYKIIDIILVNPTSSLAFFNSCLNPMVX	303
Db	254	AFALCWGPHVTSLLRAHANPGLPLVRG-----LPFVTSLAFFNSVANPVLVX	305
QY	304	FVGQDFRERLIHSLTSLRALSEDS-----APTNDTAAANSPPA	344

[illegible]

Db 254 AFALCWGPHVFSLEAHANPGLRPLVWRG-----LPTVTSIAFFNSVANPVLVY 305  
Qy 304 FVGQDFRRLIHSPTSLSERALSSEDS-----APTNDTAANSASPPA 344  
Db 306 LTCPDMRLKRLSRSLRVLESVLVDSELGAGSSRRRTSTARSASPLA 355

## RESULT 11

US-08-118-270-35  
; Sequence 35, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US-08-118-270-35

Query Match 26.4%; Score 479; DB 1; Length 304;  
Best Local Similarity 33.8%; Pred. No. 2,1e-28;  
Matches 112; Conservative 56; Mismatches 109; Indels 54; Gaps 9;  
Qy 27 ILPLVLGVGTFVLGVLGNLVIWVAGFRMTRVTTTCYLNALADFSFATLPLFLVSNMA 86  
Db 2 ILALVFAVVLGVGLGNLVVWVTAFAEKRTINAIWFLNIAVADFSLCALPILFTSIV 61  
Qy 87 MGEKPPGFQWFLCKLIHVVDINLFGSVFLIGFIADRCICVLHPVWQNHRTVSLAMKVI 146  
Db 62 QHHHPFPGGAACSLPSILLNMYASILLATISADRFLLVFKPIWQCNFRGAGLAWIAC 121  
Qy 147 VGPWTALVLTLPVLELTVTTPINGDTY-----CTENFASWGCTPEERLKVATMLTA 200  
Db 122 AVANGIALLTIPSLYRWV-----REYFPKVLGGQDISH-----DKRRERAV----- 166  
Qy 201 RGIIRFVIGFSLPMSIAICYGLIAAKIHKKGMIKSSRPLRVLTAVAVASFFFCWPPFQLV 260  
Db 167 -AIVRLVGLFWLPLTLTICY-----TTRSTKTLKVVAVAVASFFFIWLPYQVT 214

Qy 261 ALLGTWVLKEMLFYGYKIIDLIVNPTSSL-----AFFNSCLNPMLYVFGQ-DFRERLIH 315  
Db 215 GIM-----MSFLEPSSPTFLLLNKLDSLCSVCFAYINCCINPIIYVWAGQFQGRLRK 267  
Qy 316 SLPTSLERALSSEDS-----PTNDTAA 337  
Db 268 SLPSLLRNVLTEESVVRKSKSFTRSTVDTMA 298

## RESULT 12

PCT-US93-08528-35  
; Sequence 35, Application PC/TUS9308528  
; GENERAL INFORMATION:  
; APPLICANT: New York University  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08528  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US93-08528-35

Query Match 26.4%; Score 479; DB 5; Length 304;  
Best Local Similarity 33.8%; Pred. No. 2,1e-28;  
Matches 112; Conservative 56; Mismatches 109; Indels 54; Gaps 9;  
Qy 27 ILPLVLGVGTFVLGVLGNLVIWVAGFRMTRVTTTCYLNALADFSFATLPLFLVSNMA 86  
Db 2 ILALVFAVVLGVGLGNLVVWVTAFAEKRTINAIWFLNIAVADFSLCALPILFTSIV 61  
Qy 87 MGEKPPGFQWFLCKLIHVVDINLFGSVFLIGFIADRCICVLHPVWQNHRTVSLAMKVI 146  
Db 62 QHHHPFPGGAACSLPSILLNMYASILLATISADRFLLVFKPIWQCNFRGAGLAWIAC 121  
Qy 147 VGPWTALVLTLPVLELTVTTPINGDTY-----CTENFASWGCTPEERLKVATMLTA 200  
Db 122 AVANGIALLTIPSLYRWV-----REYFPKVLGGQDISH-----DKRRERAV----- 166  
Qy 201 RGIIRFVIGFSLPMSIAICYGLIAAKIHKKGMIKSSRPLRVLTAVAVASFFFCWPPFQLV 260  
Db 167 -AIVRLVGLFWLPLTLTICY-----TTRSTKTLKVVAVAVASFFFIWLPYQVT 214  
Qy 261 ALLGTWVLKEMLFYGYKIIDLIVNPTSSL-----AFFNSCLNPMLYVFGQ-DFRERLIH 315







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